

11 Publication number:

0 217 102
A1

12

EUROPEAN PATENT APPLICATION

21 Application number: 86111585.5

22 Date of filing: 21.08.86

51 Int. Cl.⁴: **C 12 N 15/00**

C 07 H 21/04, C 07 H 21/02
C 12 N 1/20, C 12 N 9/00
C 12 Q 1/00, G 01 N 33/53
C 07 K 7/10, A 61 K 39/395
/(C12N1/20, C12R1:19)

30 Priority: 28.08.85 IL 76233
08.04.86 IL 78445

43 Date of publication of application:
08.04.87 Bulletin 87/15

84 Designated Contracting States:
BE CH DE FR GB IT LI NL SE

71 Applicant: YEDA RESEARCH AND DEVELOPMENT
COMPANY, LTD.
Weizmann Institute of Science Herzl Street at Yavne Road
P.O. Box 95
Rehovot 76100(IL)

72 Inventor: Revel, Michel
Beth Brasil 5 Weizmann Institute of Science
Rehovot(IL)

72 Inventor: Chebath, Judith
Rahaz Street, 8
Rehovot(IL)

74 Representative: Patentanwälte Grünecker, Kinkeldey,
Stockmair & Partner
Maximilianstrasse 58
D-8000 München 22(DE)

54 Interferon-induced (2'-5') oligo A synthetase gene, mRNA, cDNA and enzymes having (2'-5') oligo A synthetase activity.

57 The present invention relates to a human DNA sequence coding for an enzyme having (2'-5') oligo A synthetase activity, a 1.6 kb RNA and a 1.8 kb RNA being complementary to the mentioned DNA sequences, to a DNA transfer vector, comprising an inserted DNA sequence consisting essentially of the mentioned DNA sequence, furthermore to a micro-organism which has been transformed by the said transfer vector and is capable of expressing an enzyme having the (2'-5') oligo A synthetase activity. The present invention

furthermore provides a method of monitoring the response of a patient to an interferon, which comprises measuring the concentration of (2'-5') oligo A synthetase mRNA in cells or body fluids of the patient by hybridizing the mRNA to DNA complementary thereto. In addition there are provided antigenic peptides and antibodies raised against the antigenic peptides which recognises and immunoprecipitates (2'-5') oligo A synthetase.

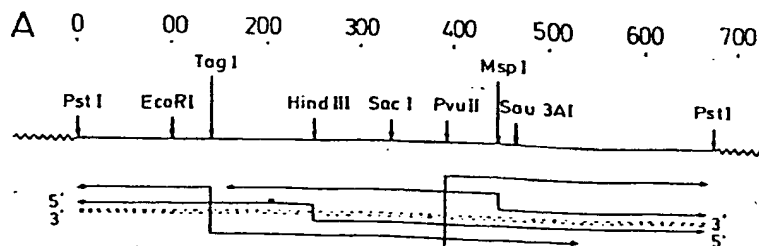


FIG. 1A

B

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30
TTT GGS AGG CTC TTG GAA TTA CTC ATA AAC TAC CAG GAA CTC TGC ATC TAC TGG ACA AAG 50
PHE ARG THR VAL LEU GLU LEU VAL TLE ASN TYR GLN GLN LEU CYS ILE TYR TRP THR LYS
90
TAT TAT GAC TTT AAA AAC CCC ATT ATT GAA AAG TAC CTG AGA AGG CAG CTC ACC AAA CCC 100
TYR TYR ASP PHE LYS ASN PRO ILE TLE GLU LYS TYR LEU ARG ARG GLN LEU THR LYS PRO 110
120
AGG CCT GTG ATC CTG GAC CCG GCG GAC CCT ACA GGA AAC TTG GGT GGT GGA GAC CCA AAG 130
ARG PRO VAL ILE LEU ASP PRO ALA ASP PRO THR GLY ASN LEU GLY GLY GLY ASP PRO LYS 140
150
GGT TGG AGG CAG CTG GCA CAA GAG GGT GAG GCC TGG CTG AAT TAC CCA TGC TTT AAG AAT 160
GLY TRP ARG GLN LEU ALA GLN GLU ALA GLU ALA TRP LEU ASN TYR PRO CYS PHE LYS ASN 170
180
TGG GAT GGS TCC CCA GTG AGC TCC TGG ATT CTG CTG GTG AGA CCT CCT GCT TCC TCC CTG 190
TRP ASP GLY SER PRO VAL SER SER TRP ILE LEU LEU VAL ARG PRO PRO ALA SER SER LEU 200
210
CCA TTC ATC CCT GCG CCT CTC CAT GAA GCT TGA GAC ATA TAG CTG GAG ACC ATT CTT TCC 220
PRO PHE ILE PRO ALA PRO LEU HIS GLU ALA 230
240
AAA GAA CTT ACC TCT TGC CAA AGG CCA TTT ATA TTC ATA TAG TGA CAG GCT GTG CTC CAT 250
260
ATT TTA CAG TCA TTT TGG TCA CAA TCG AGG GTT TCT GGA ATT TTC ACA TCC CTT GTC CAG 270
280
AAT TCA TTC CCC TAA GAG TAA TAA TAA ATA ATC TCT AAC ACC AAA 290

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FIG.1B

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10 Many of the biological effects of interferon appear to be mediated
by the induction of new mRNAs and proteins in cells exposed to IFNs
(for review: Revel, 1984; Lebleu and Content, 1982; Baglioni and Nil-
sen, 1983). Among these IFN-induced proteins two groups appear parti-
15 cularly important: 1) translation regulatory enzymes (ds RNA dependent
protein kinase and (2'-5') oligo A synthetase, (2'-5') oligo A-
activated nuclease, 2'-phosphodiesterase) and 2) cell surface anti-
gens (HLA-A, B, C, B2-microglobulin, HLA-DR). Other cellular and
excreted proteins play probably important roles as well (Weil et al,
1983; Chebath et al, 1983; Wallach et al, 1983). With the exception
20 of the HLA genes (Malissen et al, 1982; Schamboeck et al, 1983), the
structure and sometimes the function of the IFN-induced proteins is
unknown and so is the mechanism by which IFNs activate specifically
these genes. To address these questions, several cDNAs from IFN-
induced genes have been recently cloned (Chebath et al, 1983; Merlin
25 et al, 1983; Friedman et al, 1984; Samanta et al, 1984). In partic-
ular, the cDNA and gene coding for the human (2'-5') oligo A synthe-
tase was studied, a ds RNA-activated enzyme that converts ATP into
ppp(A2'pA)_n oligomers (Kerr and Brown, 1978) which in turn bind to
and activate the latent RNase F (Schmidt et al, 1978). The (2'-5')
30 oligo A synthetase is strongly induced in cells by all three types
of human IFNs, and its increase is a good marker of IFN activity
(Wallach et al, 1982). The enzyme is induced during differentiation
of hematopoietic cells, and denotes an autocrine secretion of IFN- β
(Yarden et al, 1984). The enzyme is similarly induced late in the
35 S phase of synchronized embryo fibroblasts (Wells and Mallucci,
1985). The enzyme activity drops when cell growth starts (Etienne-
Smekens et al, 1983; Creasey et al, 1983) and appears to be invol-

ved in the antigrowth effect of IFN (Kimchi et al, (1981). Deficiency in the (2'-5') oligo A synthetase or in the (2'-5') oligo A-activated RNase F have also been correlated with partial loss of the antiviral effects of IFNs (Salzberg et al, 1983; Epstein et al, 1981), although this is probably not the only mechanism by which IFN inhibits virus growth (Lebleu and Content, 1982). The (2'-5') oligo A nucleotides have been detected in many eukaryotic cells and even in bacteria (Laurence et al, 1984) and the synthetase is likely to be a wide-spread enzyme. The enzyme has been purified from mouse (Dougherty et al, 1980) and human cells (Yand et al, 1981; Revel et al, 1981); a large and a small form of the enzyme have been observed (Revel et al, 1982; St. Laurent et al, 1983) but their structures were not elucidated.

The (2'-5') oligo A synthetase, induced in cells exposed to IFNs (Hobanessian et al, 1977; Zilberstein et al, 1978) has a number of unusual properties. Its main activity is the synthesis from ATP of 5'triphosphorylated short oligo A chains (of up to 15 A, with mainly dimers to pentamers), but in contrast to other RNA polymerases, it adds adenylate or one other nucleotide specifically to the 2'OH of adenylate in oligo A (Kerr and Brown, 1978; Samanta et al, 1980), or to other (oligo)nucleotides with a free 2'OH adenylate such as NAD (Ball, 1980) or even tRNA (Ferbis et al, 1981). To be active, the enzyme has to bind to double-stranded RNA stretches of minimum 50 bp (Minks et al, 1979), and must therefore possess several binding sites: for nucleoside triphosphates, for 2'OH adenosine polynucleotides and for double stranded RNA. The enzyme binds to 2', 5' ADP-Sepharose (Johnston et al, 1980), to poly (rI)(rC)-agarose (Hovanessian et al, 1977) and to Cibacron Blue-Sepharose (Revel et al, 1981). In different cells, the (2'-5') oligo A synthetase activity is in the cytosol (Revel et al, 1981) or in ribosomal salt washes (Dougherty et al, 1980), as well as in the nuclear sap (Nilsen et al, 1982b) and even in large amounts in the nuclear matrix. It is notable that cellular RNAs can replace poly (rI)(rC) for activation of the enzyme (Revel et al, 1980) and the synthetase may even have a role in Hn RNA processing (Nilsen et al, 1982a). Some (2'-5') oligo A synthetase is bound to plasma membranes and can be incorporated in budding virions (Wallach and

- 1 Revel, 1980). These complex interactions may ensure a localized action
of the (2'-5') oligo A system (Nilsen and Baglioni, 1983) and ex-
plain its multiple suggested roles in normal and virus-infected
cells. The synthetase amounts to less than 0.1% of the proteins
5 in IFN-treated cells, and its structure could not be determined
directly.

It is possible to use measurements of (2'-5') oligo A synthetase
levels to determine whether cells in vitro or in vivo have been ex-
10 posed to IFN and respond to it. This measurement can be used as an
assay for IFN in unknown solutions, by exposing cells to said solu-
tions and determining the increase in (2'-5') oligo A synthetase
levels (Revel et al., US patent 4,302,533). The measurement can also
be used to establish whether IFN is produced in increased amounts in
15 whole organisms including man.

CLINICAL APPLICATIONS OF (2'-5') OLIGO A SYNTHETASE MEASUREMENTS

It has been established that the (2'-5') oligo A synthetase level is
20 rather constant in peripheral blood mononuclear cells (PBMC) of
healthy individuals (Schattner et al., 1981b). An increase in (2'-5')
oligo A synthetase is seen in PBMC of patients with acute viral in-
fections (Schattner et al., 1981b; Schoenfeld et al., 1985), with per-
sistent viral infections (Wallach et al., 1982), with autoimmune
25 diseases and with a number of other syndromes suspected of infectious
origin such as Jacob-Kreuzfeld disease (Revel et al., 1982). The
basal (2'-5') oligo A synthetase level is lower in granulocytes but
large increase in viral infections are seen (Schattner et al., 1984).
Increase of (2'-5') oligo A synthetase enzyme in PBMC of AIDS patients
30 was recently reported (Read et al., 1985). In animal models, it was
shown that increase in (2'-5') oligo A synthetase level is rapid and
more constant than appearance of IFN in the blood (Schattner et al., 1982a).
(2'-5') oligo A synthetase remains high for several weeks while the
IFN peak is transient.

35

The (2'-5') oligo A synthetase increases during differentiation of
haematopoietic cells as a result of autocrine secretion of IFN- β

- 1 (Yarden et al., 1984). Decreased (2'-5') oligo A synthetase levels are seen in acute leukemias with numerous blast cells (Wallach et al. 1982; Schattner et al, 1982b).
- 5 Another important application of (2'-5') oligo A synthetase measurements is in the monitoring of patients under IFN therapy. Besides clinical changes, it is possible to establish that the patients respond to IFN by measuring the PBMC (2'-5') oligo A synthetase level which increases 5-10 fold during systemic IFN- α as well as β treatment
- 10 (Schattner et al., 1981a, Schoenfeld et al., 1984). It is clear that assay of other IFN-induced activities or molecules can be used as well as the assay of the (2'-5') oligo A synthetase enzyme, but this method has been the most widely used (Read et al., 1985; Merritt et al., 1985). In all these studies, the enzymatic assay measuring
- 15 the conversion of ATP into (2'-5') (A)_n oligomers has usually been employed. (Revel et al., US patent 4,302,533).

To detect the (2'-5') oligo A synthetase anti-(2'-5') oligo A synthetase peptide antibodies can be used. For the obtaining of

20 antibodies to (2'-5') oligo A synthetase, peptide sequences can be chosen from the total amino acid sequences of different (2'-5') oligo A synthetases, to serve as antigens for the induction of antibodies against the native (2'-5') oligo A synthetase molecule. Rabbits were injected subcutaneously with the antigenic peptides in order to pro-

25 duce the antibodies. Subsequent boostings were done and continued until maximal antibody response.

The present invention concerns human DNA encoding an enzyme having (2'-5') oligo A synthetase activity. One form of the DNA has the

30 nucleotide sequence set forth in Figure 7A. Another form of the DNA has the sequence of nucleotides 1-1322 set forth in Figure 7A which overlaps with the sequence of nucleotides 901-1590 set forth in Figure 7B.

- 35 An enzyme having (2'-5') oligo A synthetase activity has the amino acid sequence set forth in Figure 7A. Another enzyme having (2'-5')

- 5 -

1 oligo A synthetase activity has the sequence of amino acids 1-364 set forth in Figure 7A which overlaps with the sequence of amino acids 290-400 set forth in Figure 7B.

5 A 1.6 kb and 1.8 kb RNA having nucleotide sequences complementary to the nucleotide sequences in Figures 7A and 7B have been isolated.

A method of monitoring the response of a patient to an interferon comprises measuring the concentration of (2'-5') oligo A synthetase mRNA
10 in cells or body fluids of the patient by hybridizing to the mRNA DNA complementary thereto.

Antigenic peptides of the present invention have an amino acid sequence contained within the amino acid sequences set forth in
15 Figures 7A and 7B. Antibodies raised against these antigenic peptides recognize and immunoprecipitate (2'-5') oligo A synthetase.

A method of monitoring interferon activity in a subject comprises measuring the amount of (2'-5') oligo A synthetase in a cell or body
20 fluid of the subject at predetermined time intervals, determining the differences in the amount of said synthetase in the cell or body fluid of the subject within the different time intervals, and determining therefrom the amount of synthetase in the cell or body fluid of the subject and thereby the interferon activity of the subject.
25 The synthetase may be measured by contacting the synthetase with an antibody of the present invention so as to form a complex therewith and determining the amount of complex so formed.

Furthermore, the present invention concerns two antibodies for (2'-5')
30 oligo A synthetase which can be obtained by preparing antigens which comprise a partial amino acid sequence of (2'-5') oligo A synthetase. The anti-(2'-5') oligo A synthetase peptide antibodies can be used to detect the enzyme.

1 Brief description of the Figures

Figure 1 depicts the structure and sequence of (2'-5') oligo A synthetase E₁ cDNA clone 174-3:

5

Figure 1A depicts the restriction map of E₁ cDNA clone 174-3. The insert base pairs are numbered in the same direction as pBR322 DNA. The pBR Eco R1 site is on the right. Both strands of the insert (dotted lines) were sequenced (Maxam & Gilbert, 1980) from the restriction sites indicated by the vertical lines. The coding strand is 5' to 3' from right to left. Following the right Pst1 site there were 17G and 72T, followed by the dinucleotide GA and the 3T of the sequence shown in (B) which are therefore not part of the tails. At the 3' end, tails of 45A and 10C preceded the left Pst 1 site.

10

15

Figure 1B depicts the nucleotide sequence having the longest coding frame. The first T is nucleotide 92 following the tails of the insert (right end in A). The Sau 3A₁ site and the Eco R1 of the insert are at positions 129 and 480 respectively of the sequence shown.

20

Figure 2 depicts the size and induction of E₁ specific mRNAs in SV80 and Namalva cells:

25

Figure 2A depicts the hybridization of nick translated [³²P]-cDNA of clone E₁ to electrophoretic blots of denatured poly A⁺-RNA from SV80 cells. The RNAs were prepared at the indicated hour after IFN-beta-1 addition. The apparent size of the RNA is indicated on the autoradiography. Left lane, rRNA markers.

30

Figure 2B is the same as 2A with RNA from Namalva cells treated with IFN-alpha for the indicated time. Left lane: rRNA markers.

35

- 1 Figure 3 depicts the characterization by hybridization to RNA blots of recombinant plasmid clone C56, harbouring cDNA for an IFN-induced mRNA Poly(A)⁺ RNA from IFN-treated SV80 cells (I) or from non-treated cells (C), 7 micrograms were electrophoresed on agarose gels and
- 5 after blotting to nitrocellulose were hybridized to nick-translated [³²P]-plasmid DNA of either the C56 clone, a human HLA cDNA clone or a rat tubulin cDNA clone. Exposure was for 48 h. Position of radioactive 18S of ribosomal RNA marker is indicated.
- 10 Figure 4 depicts the partial restriction map and nucleotide sequence of the C56 450 bp insert. The C56 plasmid was digested with Hind 3, end-labelled with alpha-[³²P]-dCTP by the DNA polymerase I-large fragment (Klenow enzyme, Boehringer) and the Hind 3 - Pst 1 fragments were separated on a 1% agarose gel. In order to sequence the comple-
- 15 mentary strand, the plasmid was 5'-labelled at the Bgl2 site with gamma [³²P]-ATP by the T₄-polynucleotide kinase (Biolabs) and the Bgl 2 - Pst 1 fragments were isolated. Sequencing was made by the Maxam and Gilbert technique. Sequence of coding strand A (right to left) is shown in the lower panel. The two first thymidylic residues of
- 20 the sequence of strand A probably correspond to the AT tail as indicated in the upper diagram.

Figure 5 depicts the time course of the induction of C56 mRNA by IFN:

- 25 Figure 5A depicts Poly (A)⁺RNA, 7 micrograms, from Namalva cells treated with IFN-alpha 1000 U/ml for the indicated times were electrophoresed on agarose gels and, after blotting, were hybridized with nick-translated [³²P]-C56 plasmid DNA.
- 30 Figure 5B depicts Poly (A)⁺RNA, 7 micrograms, from SV80 cells treated with 200 U/ml IFN-beta for the indicated times. The asterisk indicates an RNA sample from cells treated with IFN-beta-1 purified on monoclonal antibody column (2x10⁸ U/mg).
- 35 Figure 5C depicts Poly (A)⁺RNA, 1 microgram, from SV80 cells treated as in (5B), was hybridized in liquid with 3' end-labelled fragment I of C56 DNA (see Fig. 4). The hybrids were treated

1 with S_1 -nuclease and analyzed on denaturing gels. The mRNA-hybridized probe (—→) is shorter than the self-reassociated probe (----→).

5 Figure 6 depicts the restriction map of cDNAs for the 1.6 and 1.8 kb (2'-5') oligo A synthetase mRNAs.

10 Figure 6A depicts the map of the 1.6 kb cDNA. The position of the E1 cDNA (Merlin et al., 1983) and of the lambda gt 10 cDNAs is shown. pA is the polyadenylation site. The exon limits are shown by vertical dotted lines. The size of the genomic DNA fragments carrying each exon are given in parentheses. The vertical arrow shows the position of the additional splice site in the 1.8 kb RNA. The strategy for sequencing the 9-21 and 15 5-21 cDNAs is indicated. The sequence from the 3' Eco R1 site (E) to the Pst 1 site (P) was determined in the E1 cDNA (Merlin et al., 1983).

20 Figure 6B depicts a map of the 1.8 kb cDNA. the lambda gt10 clone 48-1 was isolated using the Pst1-Pst1 genomic fragment containing exon 8 of the 1.8 kb RNA (Fig. 9). Exons are numbered as for the 1.6 kb E cDNA. The truncated exon 7 is designated 7a.

25 Figures 7A and B depict the nucleotide sequences of the two (2'-5') oligo A synthetase cDNAs. The nucleotides of the 1.8 kb cDNA clone 48-1 are numbered as for the 1.6 kb cDNA clone 9-21. Amino acid numbering is given in parantheses. Translation starts at the first or second codon of the ATGATG sequence. Limits between exons are 30 shown by vertical bars. (Glycos.) indicates a possible glycosylation site in E18. Single base variations, possibly allelic differences, were detected between clones or genomic DNA in the 1.6 kb sequence at 376 (T for C), 525 (G for A), 807 (G for C), 811 (A for G); in the 1.8 kb sequence at 1087 (G for A), 1115 (G for C).

35 Figure 8 depicts the hydropathy plot of the C-termini of the E16 and E18 (2'-5') oligo A synthetases. The computer program of Kyte and

1 Doolittle (1982) was used. Hydrophobic regions are over the midline.
The acidic region in E18 corresponds to amino acids 353 to 358 in
Figure 7.

5 Figure 9 depicts the restriction map of the human (2'-5') oligo A
synthetase gene. A map constructed from three overlapping genomic
clones is shown with the position of the 7 exons of the 1.6 kb RNA
and the additional 8th exon of the 1.8 kb RNA (black bars). The
insert shows a Southern blot of genomic DNA with the 48-1 cDNA as
10 probe. Slot 1, Daudi DNA; slot 2, diploid fibroblast FS11 DNA.

Figure 10 depicts the promoter region of the human (2'-5') oligo A
synthetase gene. A restriction map of the Sph1-Sph1 0.85 kb fragment
from the 4.2 kb EcoR1 genomic DNA segment in Figure 9 is shown. The
15 5' end of the mRNAs is marked as cap.

Figure 11 depicts the sequence of the human (2'-5') oligo A synthetase
promoter region. The sequence of the Sau3a-Hpa1 segment shown in
Figure 10, aligned for comparison with the promoter region of the
20 human IFN-beta-1 gene (Degraeve et al., 1981). Numbering is from the
presumed cap site. A purine rich transcription regulatory sequence
around -75 in the IFN-beta-1 promoter (Zinn et al., 1983), repeated
at -10, is underlined. The TATA box is doubly underlined.

25 Figure 12 depicts the SDS-acrylamide gel electrophoresis of ³⁵S-
methionine labelled proteins from IFN treated WISH cells immuno-
precipitated by antiserum to synthetic peptides.

Figure 13 depicts the expression of E16 cDNA in E. coli. Extracts of
30 E. coli lysogen Agt11-E16 induced by IPTG at 42°C were assayed on
poly (rI) (rC) agarose beads for (2'-5') oligo A synthesis. Cont =
extracts of E. coli with E16 cDNA in opposite orientation to lac Z
gene. Nam = extracts of IFN-treated Namalva cells. Electrophoresis
at pH 3.5 of alkaline phosphatased ³²P-a-ATP labelled products are
35 shown.

1 Figure 14 depicts the rapid method for assay of (2'-5') oligo A
synthetase RNAs in human peripheral white blood cells.

Figure 15 depicts the quick cell blot for (2'-5') oligo A synthetase
5 E RNAs in human PBMC according to the method of Figure 14. Indicated
number of cells and IFN (16 H treatment) were used. Autoradiography
with ^{32}P -cDNA.

Figure 16 depicts the (2'-5') oligo A synthetase activity which is
10 adsorbed on anti-B and anti-C IgG-Protein A-Sepharose was measured as
described in Example . The scheme underneath shows the position of
peptide B and peptide C in the two (2'-5') oligo A synthetase forms
E16 and E18 sequenced by Benech et al. (1985b). The blackened area
indicates the part of E18 which differs from the E16 molecule.

15

Figure 17 depicts electrophoresis and immunoblotting of extracts
from human cells as described in Example 2. The position of the 4
forms of (2'-5') oligo A synthetase is indicated by the numbers on the
right of each blot. M = ^{14}C -protein molecular weight markers. IFN
20 treatment is indicated by +.

Figure 18 depicts electrophoretic immunoblots of extracts from human
SV80 cells with anti-(2'-5') oligo A synthetase peptide B. Left:
crude cytoplasmic extract (S1.5), cell sap (S100) and Microsomes
25 (P100). Right: Na deoxycholate 10% extract of microsomes (DOC-soluble),
high salt wash of microsomes (RWF) and microsomal pellet after salt
extraction (Microsomes-KCl).

Figure 19 depicts the fractionation of S100 and high-salt wash of
30 microsomes (RWF) on DEAE-cellulose and carboxymethyl-cellulose,
followed by glycerol gradient. The (2'-5') oligo A synthetase profile
and protein detected by anti-B are shown below the gradients. Electro-
phoretic immunoblot show fraction CM (CM-cellulose eluate from the
S100 proteins non-adsorbed to DEAE-cellulose) on the left blot. On
35 the right-hand blot fraction, DE (DEAE-cellulose eluate of RWF) and
fraction GG (heavy peak of 80-100 kd from glycerol gradient of fraction
DE).

1 Figure 20 depicts the double stranded RNA requirements of various forms of (2'-5') oligo A synthetase from SV80 cells. Fractions are labelled as in Figure 19. Enzymatic activity measured at indicated concentrations of poly (rI)(rC).

5

Figure 21 depicts the radio-immunoassay of (2'-5') oligo A synthetase with anti-B IgG and ¹²⁵I-Protein A as described in Example 3. Autoradiography is shown. Cells treated for 16 hours with 500 U/ml IFN-β1 or left untreated.

10

Figure 22 depicts the use of anti-B for immunofluorescence microscopic detection of elevated (2'-5') oligo A synthetase levels in lymphocytes from blood of patient with viral disease (middle panel). Right: control with normal serum: left: blood from healthy donor with anti-B

15 stain. (Lymphocytes do not stain, only macrophages or granulocytes give unspecific background).

Detailed description of the invention

20 The present invention concerns human DNA encoding an enzyme having (2'-5') oligo A synthetase activity and having the nucleotide sequence set forth in Figure 7A. The DNA may also comprise the sequence of nucleotides 1-1322 set forth in Figure 7A and the overlapping sequence of nucleotides 901-1590 set forth in Figure 7B. The DNA of the
25 present invention has the restriction enzyme sites set forth in Figure 9.

An enzyme having (2'-5') oligo A synthetase activity has the amino acid sequence set forth in Figure 7A. This enzyme comprises about
30 364 amino acids and has a molecular weight of about 41,500 daltons. another enzyme having (2'-5) oligo A synthetase activity comprises the sequence of amino acids 1-364 set forth in Figure 7A and the sequence of amino acids 290-400 set forth in Figure 7B. This enzyme comprises about 400 amino acids and has a molecular weight of about 46,000
35 daltons.

- 1 The present invention provides a 1.6 kb RNA having a nucleotide sequence complementary to the nucleotide sequence set forth in Figure 7A. Also provided is a 1.8 kb RNA comprising a nucleotide sequence complementary to the sequence of nucleotides 1-1322 set forth in
5 Figure 7A and the sequence of nucleotides 901-1590 set forth in Figure 7B.

A transfer vector of the present invention comprises lambda-gt 11-E16 DNA of the present invention, and the lac Z gene, the DNA being fused
10 in phase with the lac Z gene, so as to enable expression of the DNA in a suitable host cell. A microorganism may be transformed by the transfer vector. Escherichia coli is a suitable microorganism for the transformation.

- 15 A method of monitoring the response of a patient to an interferon comprising measuring the concentration of (2'-5') oligo A synthetase mRNA in cells or body fluids of the patient by hybridizing to the mRNA DNA complementary thereto. The mRNA may be the 1.6 kb or 1.8 kb RNA of the present invention.

20

A method for evaluating the response of cells and tissues to interferon comprises hybridizing RNA from cells or tissues exposed to interferon with cDNA complementary to the RNA, and determining the extent of hybridization. The RNA is extracted from cells or tissues
25 which have been exposed to interferon, immobilized on a membrane filter and hybridized to labelled cDNA specific for interferon-induced mRNAs. The method may also comprise in situ hybridization of labelled cDNA to slices of tissues and then evaluating by microscopic examination autoradiography, or fluorescence. The cells or tissues analyzed
30 may be of human or other animal origin.

A kit for carrying out a method for evaluating the response of cells and tissues to interferon contains a cDNA complementary to a sequence set forth in Figure 7A or 7B, reagents to carry out the hybridization
35 tests for nick-translation with deoxyribonuclease I and [³²P]-gamma-dCTP, reagents for hybridization on nitrocellulose membranes, and reagents for RNA extraction from cells.

1 Also provided are antigenic peptides having amino acid sequences contained within the amino acid sequences set forth in Figure 7A and Figure 7B.

5 An antigenic peptide of the present invention has the amino acid sequence comprising the 17 C-terminal amino acids of the amino acid sequence set forth in Figure 7A and having the amino acid sequence: ARG-PRO-PRO-ALA-SER-SER-LEU-PRO-PHE-ILE-PRO-ALA-PRO-LEU-HIS-GLU-ALA:

Another antigenic peptide has the amino acid sequence: GLU-LYS-TYR-
10 LEU-ARG-ARG-GLN-LEU-THR-LYS-PRO-ARG-PRO-VAL-ILE-LEU-ASP-PRO-ALA-ASP.

Antibodies raised against the antigenic peptides of the present invention recognize and immunoprecipitate (2'-5') oligo A synthetase.

15 A method of monitoring interferon activity in a subject comprises measuring the amount of (2'-5') oligo A synthetase in a cell or body fluid of the subject at predetermined time intervals, determining the differences in the amount of said synthetase in the cell or body fluid of the subject within the different time intervals, and deter-
20 mining therefrom the amount of synthetase in the cell or body fluid of the subject and thereby the interferon activity of the subject. The amount of synthetase may be measured by contacting the synthetase with an antibody of the present invention so as to form a complex therewith and determining the amount of complex so formed.

25 A method of monitoring interferon activity may further comprise the extraction of (2'-5') oligo A synthetase from a cell or body fluid which has been exposed to interferon, labelling the extracted synthetase with an identifiable marker to form a labelled synthetase, contacting the labelled synthetase with an antibody of the present
30 invention under suitable conditions so as to form a labelled synthetase-antibody complex, and detecting the marker in the complex, thereby detecting the synthetase. The marker may be ³⁵S-methionine.

A kit for carrying out the method of monitoring interferon activity
35 comprises an antibody of the present invention, materials for extracting the synthetase, materials for labelling the synthetase, and materials for detecting the marker and determining the amount of synthetase.

1 The present invention also provides cloned DNA that specifically
hybridizes to messenger RNAs which appear in human cells after exposure
to interferon. The cloned cDNA may be specific for the (2'-5') oligo
A synthetase mRNAs of 3.6, 1.8 and 1.6 kilobase. A cloned DNA of the
5 present invention is specific for the mRNA of a 56,000 Mr-protein,
which mRNA is 2 kilobase and which has the sequence defined in Figure
1.

A partial cDNA clone (E1) for the (2'-5') oligo A synthetase mRNA
10 from human SV80 cells, was first obtained through its ability
to select by hybridization a mRNA producing (2'-5') oligo A synthe-
tase activity upon translation in *Xenopus laevis* oocytes (Merlin
et al, 1983). The E1 cDNA insert (675 bp) hybridizes to 3 RNA
species of 1.6, 1.8 and 3.6 kb which are coinduced by IFN in SV80
15 cells, accumulate for 12 hours and are found in the cytoplasmic
polysomal fraction (Benech et al, 1985). Two other early transcripts
(2.7 and 4 kb) appear in lesser amounts. Analysis of various types
of human cells has shown that these RNAs are differentially expres-
sed in a cell specific manner. In B lymphoblastoid cells (Namalva,
20 Daudi) only the 1.8 kb RNA accumulates, while in amniotic WISH
cells, in histiocytic lymphoma U937 cells and in HeLa cells, the
1.6 kb RNA is predominantly induced by IFN with some 3.6 kb RNA
but little 1.8 kb RNA. In diploid fibroblasts FS11, in SV80
fibroblastoid cells and in the T cell line CEMT, all 3 stable
25 RNAs are expressed (Benech et al, 1985). The type of (2'-5')
oligo A synthetase RNA expressed does not depend on the species of
IFN used (α , β or μ) but rather seems developmentally regula-
ted in the cell.

30 The different (2'-5') oligo A synthetase transcripts appear to
originate from a single gene (Benech et al, 1985). Restriction
mapping showed 1) that the E1 cDNA corresponds to the 3' end of the
1.6 kb RNA, 2) that the 1.8 kb RNA has a different 3' end than the
1.6 kb RNA and contains an additional downstream exon, 3) that the
35 3.6 kb RNA has the same 3' end as the 1.8 kb RNA but is incompletely
spliced. Hybridization-translation experiments using specific genomic
DNA fragments also demonstrate that both the 1.8 and 1.6 kb RNAs
actively code for (2'-5') oligo A synthetase (Benech et al, 1985).

1 cDNA clones for the 1.6 and 1.8 kb RNAs have been isolated and sequenced, which enabled the deduction of the amino acid sequences of two forms of the IFN-induced (2'-5') oligo A synthetase in human cells. The two proteins differ in their C-termini, which is hydrophobic in the 1.6 kb RNA product (E16) and acidic in the 1.8 kb RNA product (E18). A complete mapping of the (2'-5') oligo A synthetase gene shows that the 1.6 kb RNA is coded by 7 exons and the 1.8 kb RNA by 8 exons. The sequence of the presumed transcription initiation site and promoter region of the IFN-activated human (2'-5') oligo A synthetase gene shows a striking homology to the promoter region of the human IFN- β 1 gene.

EXAMPLE 1

MEASURE OF (2'-5') OLIGO A SYNTHETASE mRNA by cDNA CLONES

15 A) Isolation of E-cDNA clones

Total RNA was prepared from 10^9 SV80 cells (SV40-transformed human fibroblasts) treated for 12 hours with 200 units per ml IFN-beta. The RNA was extracted by 3M LiCl -6M urea and purified by passage on
20 oligo dT-cellulose. The 0.4 mg poly A⁺-RNA obtained were fractionated in a preparation of gel electrophoresis apparatus in 1.5% agarose/6M urea 25mM sodium citrate pH 3.5. The 17-18S RNA fraction, was used to prepare cDNA as follows: 2 micrograms RNA were heated for 1 min at 90°C with 2 micrograms oligo (dT)₁₂₋₁₈ in 60 microliters water, cooled at 0°C, supplemented with salts to a final concentration of 50mM Tris-HCl pH 8.3, 10mM MgCl₂, 75mM KCl and incubated 5 min at 42°C before adding 1mM dithiothreitol, 1mM each dATP, dTGP, 0.5mM dCTP, 20 micro-Ci ³²P-dCTP (300 (Ci/mmol)), 4mM Na-pyrophosphate and 20 units reverse transcriptase in a final volume of
25 0.1ml. The mixture was incubated for 45 minutes at 42°C, the reaction was stopped with 10mM EDTA, 0.2% Na-dodecyl sulfate and the cDNA extracted with phenol-chloroform, treated with 0.3N NaOH for 2 hours at 52°C and neutralized. The cDNA was filtered on Sephadex G-75, ethanol precipitated, and tailed by dATP with terminal transferase. The synthesis of the second cDNA strand was primed with
35 oligo (dT) and carried out as for the first strand for 2 hours at 42°C but without radioactive nucleotide and without pyrophosphate. To insure blunt ends the ds cDNA was incubated with E. coli DNA

- 1 polymerase I large fragment first in 20mM Tris-HCl pH 8, 75mM KCl, 5mM MgCl₂, 1mM dithiothreitol for 5 minutes at 37°C (trimming reaction) and then under the conditions of filling-in with ATP. The ds cDNA was fractionated by sedimentation on a 5-20% sucrose gradient and
- 5 the heaviest fractions were tailed with dCTP and annealed with equimolar amounts of PstI-cut pBR322 plasmid DNA tailed with dCTP. About 7 ng DNA were mixed with 100 microliters of frozen, CaCl₂-treated, E. coli MM294. After 30 minutes at 0°C, and 5 minutes at 37°C, the bacteria were grown in 2ml of LB-broth for 2 hours at 37°C, and
- 10 plated on LB-agar plates with 10 micrograms/ml tetracycline. About 1.4×10^5 tetracycline-resistant, ampicillin-sensitive colonies were obtained per microgram recombinant plasmid DNA.

- To identify the cDNA clone of the (2'-5') oligo A synthetase mRNA,
- 15 a total of 3,000 plasmid DNA clones were screened by hybridization to RNA of IFN-treated SV80 cells, and the DNA-selected RNA was tested by injection into Xenopus laevis oocytes and a measure of the (2'-5') oligo A synthetase activity formed according to the method of Shulman and Revel (1980). Pools of plasmid DNA from 12 individual clones (3
- 20 micrograms DNA each; cut with Eco RI) were applied onto a 0.4cm diameter nitrocellulose filter and prehybridized for 2 hours at 37°C in 50% formamide, 2mM Pipes buffer pH 6.4, 0.75M NaCl, 1mM EDTA (buffer A). Three filters with pBR322 DNA and thirty filters of recombinant DNA pools were incubated together with 300 micrograms poly A⁺-RNA
- 25 (calculated to have a 10-fold excess of each insert cDNA over the presumed amount of (2'-5') oligo A synthetase mRNA, 0.09 micrograms or 0.03%) in 1ml buffer A for 20 hours at 37°C. The filters were washed twice at 37°C with buffer A, 4 times in 20mM Tris-HCl pH 7.5, 0.15M NaCl, 1mM EDTA, 0.5% Na dodecyl sulfate (once at 37°C and 3
- 30 times at 52°C) and then 4 times with 10mM Tris-HCl pH 7.5, 1mM EDTA (buffer C) at 52°C. Each filter was next washed individually in buffer C at 52°C and the RNA was eluted by heating 2 min at 96°C in 0.3ml buffer C with 40 micrograms rabbit liver tRNA per ml. After quick cooling the ethanol precipitation, the RNA was dissolved in 2
- 35 microliters water. Ten Xenopus laevis oocytes were microinjected with 0.7 microliters RNA and after 18 hours at 19°C, the oocytes were homogenized in their incubation medium (Shulman and Revel, 1980) and 0.15 ml of homogenate was mixed with poly (rI) (rC)-agarose beads.

1 The beads were incubated for 16 hours at 30°C with 2.5 mM (³²P)-
 alpha-ATP (0.3 Ci/mmol), 10 mM dithiothreitol, and 10 microliters of
 the liquid phase were incubated with 0.35 units bacterial alkaline
 5 phosphatase in 30 mM Tris-base for 60 minutes at 37°C. The digest
 was submitted to paper electrophoresis on Whatman 3MM paper at 3,000
 V for 4 hours, and the spots corresponding to (2'-5') ApA and (2'-5')
 ApApA were cut and counted by scintillation. From the DNA-selected
 RNA, 1 microliter was used for in vitro translation in a reticulocyte
 lysate as described in Weissenbach et al. (1979), to measure the
 10 total mRNA activity of the sample.

The ratio of (2'-5') oligo A synthetase activity over total mRNA act-
 ivity in the DNA-selected RNA samples was calculated for each filter.
 One filter with pool 174, out of the 250 pools of 12 individual plas-
 15 mids, gave consistently a ratio about 10 times higher as other pools
 or as pBR322 DNA. The plasmid DNA of each individual clone of pool
 174 was tested on separate filters and clone 174-3 was found to give
 consistently a 35-100 fold enrichment of the (2'-5') oligo A synthe-
 tase mRNA over total mRNA as compared to total RNA or pBR322 DNA-sel-
 20 ected RNA (Table 1). Clone 174-3 was identified as the (2'-5')
 oligo A synthetase cDNA and designated E-cDNA. The structure and
 sequence of this cDNA is shown in Fig. 1. The E-cDNA clone contains
 the sequence for the 100 carboxy terminal amino acids of the enzyme
 and a 192 nucleotide-long untranslated region preceding the poly A-
 25 tail.

TABLE 1

IDENTIFICATION BY HYBRIDIZATION-TRANSLATION OF THE CLONE OF (2'-5')
 OLIGO A SYNTHETASE cDNA

30 E mRNA activity measured by oocyte injection (2) of induced RNA

	Ept. 1		Ept. 2		Ept. 3	
	(2'-5')		(2'-5')		(2'-5')	
	oligo A (specific cpm activity)*		oligo A (specific cpm activity)*		oligo A (specific cpm activity)*	
35 Total poly A ⁺ -RNA	4050	(0.007)	3440	(0.004)	4900	(0.01)

1	RNA selected on:					
	pBR filters	350		570	(0.03)	670
		625	(0.05)	595		725
	plasmid pool 174	2320		-		-
	other pools	230**		-		-
		230:60		-		-
5	Clones of pool 174:	1	560	700		995
		2	625	950	(0.04)	825
		3	6460	39,800	(2.7)	11,235
		4	600	1,820	(0.48)	1,030
		5	745	500	(0.19)	530
		6	985	475		630
		7	1270	365		605
		8	395	800	(0.02)	600
		9	490	100		1,030
		10	1465	290		1,155
		11	1860	365		735
		12	540	320		915
15	No RNA	195		185		590

*Specific activity ratio of (2'-5') oligo A synthesis in mRNA-infected oocytes to translation of same RNA in reticulocyte lysates.

** Average of 28 pools.

20 B) MEASURE OF INTERFERON-INDUCED (2'-5') OLIGO A SYNTHETASE mRNA
BY HYBRIDIZATION OF E-cDNA.

Plasmid DNA of clone 174-3 (E-cDNA) can be used to detect the complementary RNA on electrophoretic blots of total cell RNA. Poly A⁺-RNA
 25 is prepared from SV80 cells treated various times by 2000/ml interferon-beta and 7 micrograms RNA are denatured in 50% formamide, 6% formaldehyde, electrophoresed in 1.3% agarose with 6% formaldehyde and blotted onto nitrocellulose according to the procedures of Thomas (1980) and Fellous et al. (1982). The E-cDNA plasmid labeled by
 30 nick-translation with (³²P)-gamma-dCTP according to Merlin et al. (1983), is hybridized to the nitrocellulose blot.

In SV80 cells, three RNA species which are all coordinately induced by the interferon treatment, hybridize with E-cDNA (Fig. 2), a
 35 large RNA species of 3.6 kilobases and 2 smaller species of 1.85 and 1.65 kilobase. In non-treated SV80 cells, no E-specific RNA is found. The 3 RNA species appear at 4 hours, are maximum at 12 hours and decrease slowly thereafter. The RNAs are still clearly detected

1 at 24 hours after interferon. Additional RNA species seen only at 4
hours are most probably precursors of the more stable species. The
same 3 RNA species are seen in human diploid fibroblasts treated by
interferon. However, in cells of the hemopoietic lineage such as
5 lymphoblastoid Namalva cells, only one main RNA species hybridizes to
E-cDNA (Fig. 2) and corresponds to the 1.85 kilobase RNA species.
The same RNA pattern is seen in other lymphoblastoid cells, in ery-
throid HL-60 and in promonocyte U937 cells.

10 The different E-specific RNA pattern in fibroblasts and lymphoid
cells corresponds to different forms of the (2'-5') oligo A synthe-
tase in these cells. Lymphoid cells contain an enzyme of molecular
weight 30,000 daltons, while fibroblasts contain two forms of the
enzyme of molecular weight 80,000 and 30,000 daltons, as reported by
15 Revel et al. (1982). The small 1.85 kilobase mRNA is sufficiently
long to code for the 30,000 Mr enzyme but not for the larger form,
while the 3.6 kilobase E-mRNA codes for the 80,000 Mr form of the
enzyme. All three E-specific RNA species hybridize to a single clone
of human genomic DNA, and probably originate from a single gene, the
20 3.6 kilobase RNA having an additional interferon exon as compared to
the 1.85 kilobase RNA.

Leucocyte interferon-alpha induces E-specific RNA as well as does
fibroblast interferon-beta. The multiplicity of RNA species revealed
25 by hybridization to E-cDNA suggests that different interferon
species, which all induce (2'-5') oligo A synthetase, could induce
different forms of the RNA and of the enzyme. Different interferon
species can also vary in their efficacy for inducing E-mRNA.

30 RNA to be treated in the above hybridization assay to E-cDNA may be
prepared from various cells in culture or from tissues taken from
patients receiving interferon therapy or suffering from viral dis-
eases or from disease in which an elevated (2'-5') oligo A synthetase
was observed (Schattner et al., 1981). Rna may also be prepared from
35 blood cells, such as leukocytes, obtained from peripheral blood. The
electrophoretic blot can be replaced by a dot-hybridization method,
in which RNA samples are directly applied to nitrocellulose in cir-
cles or rectangles of defined area, and the radioactive cDNA is hyb-

- 1 ridized to the nitrocellulose sheet. The radioactivity of each circle or rectangle is then measured by direct counting or by autoradiography followed by screening of the autoradiographic film.
- 5 An alternative method is to perform hybridization in situ on tissue slices obtained from biopsies of tissues exposed to interferon. This can be preferentially applied to brain biopsies in patients receiving interferon for a brain viral disease or tumor, in order to measure whether the brain has been exposed to interferon when the drug is
- 10 given either by intrathecal injection or by systemic injection. The method may be applied to skin biopsies when the interferon treatment is given locally as an ointment for skin lesions. It is obvious that many other applications are possible. The tissue slices may be fixed and hybridized in situ to radioactive DNA, followed by an autoradiography with a sensitive photographic emulsion. The cDNA may also be
- 15 labeled by fluorescent nucleotides or by modified nucleotides which can bind fluorescent molecules, and the hybridization to the tissue slice can be monitored by fluorescent microscopy.
- 20 An increase in hybridization of the E-cDNA was compared to a proper control cell RNA or tissue sample, indicating that the cell or tissue has been exposed to interferon. The rapidity (4-24 hours) and sensitivity (1-200 units of interferon per ml) of the method makes it very useful to follow a treatment by external interferon, or formation of endogenous interferon in blood and tissue of patients.
- 25

EXAMPLE 2

CLONED cDNA FOR THE INTERFERON-INDUCED 56,000 Mr PROTEIN

A) Isolation of cloned C56-cDNA

30

The cloned cDNA was isolated from the library of recombinant plasmids described in Example 1. The principle of the method used was differential hybridization. Two duplicate sets of the 3,000 bacterial clones grown on nitrocellulose filters were hybridized either to

35 (³²P)-cDNA from 17S-18S poly A⁺-RNA of SV80 cells treated by interferon-beta (200 U per ml), or to (³²P)-cDNA from total poly A⁺-RNA of non-treated SV80 cells. The radioactive cDNA were reverse transcribed from mRNA as in Example 1. About 40% of the bacterial clones

1 hybridized strongly to the "interferon-treated" cDNA probe and 8%
gave a clear differential signal, hybridizing preferentially or un-
iquely to the "interferon-treated" cDNA as compared to the "non-
treated" cDNA. The latter group of clones was then screened by hyb-
5 ridizing the plasmid DNA from each clone, labeled radioactively by
nick-translation, to electrophoretic blots of RNA from interferon-
treated SV80 cells and from non-treated cells. By this criterion,
1-2% of the original 3,000 bacterial clones were found to contain a
plasmid cDNA clone corresponding to an interferon-induced mRNA. One
10 of these plasmid cDNA clones, designated C56, showed a particularly
strong differential hybridization. This C56 DNA hybridizes to an
18S RNA present in interferon-treated cells but completely absent
from control cell RNA (Fig. 3). In comparison, HLA-A,B,C mRNA which
is increased 5-fold in SV80 cells after interferon-treatment
15 (Fellous et al., 1982), appears much less induced than C56 mRNA and
under the experimental conditions of Fig. 3, gives a clear signal
also with "non-treated" RNA.

The mRNA selected by hybridization to C56 cDNA immobilized on nitro-
20 cellulose filters, followed by elution from the films (as in Exam-
ple 1) was translated in a reticulocyte lysate cell-free system and
the (³⁵S)-methionine-labeled translation products were analyzed by
polyacrylamide gel electrophoresis in Na-dodecyl sulfate according to
the method described in Weissenbach et al. (1979) adapted from
25 Laemle (1970). The C56 cDNA-selected RNA is translated into a
56,000-Mr protein. The sequence of the C56 cDNA permits one skilled
in the art to deduce 65 amino acids of the carboxy terminal sequence
of the 56,000 Mr protein (Fig. 4).

30 Hybridization of the C56 cDNA to RNA extracted from SV80 cells treat-
ed various times by interferon-beta (200 U per ml), shows that the
C56 mRNA starts to appear at 1 hour after interferon addition
(Fig. 5). The C56 RNA reaches its maximum after 4 hours, but is
still detectable, although reduced, at 24 hours. Induction of C56
35 mRNA was also demonstrated in diploid fibroblasts, and in lymphoblast-
oid cells. Induction was proportional to the concentration of inter-
feron between 10 and 200 units per ml. C56 mRNA was also induced by
interferons alpha and gamma, although the latter was less efficient.

1 The absence of this mRNA in non-treated cells and its strong and
rapid increase after interferon addition make the C56 cDNA an excell-
ent probe to evaluate the response of cells to interferon. The tech-
niques described for E-cDNA in Example 1, can be similarly applied to
5 the C56 cDNA.

The availability of a number of cDNA corresponding to mRNA induced by
interferon offers new perspectives. In particular, interferon is
needed at 100-fold lower concentrations to induce HLA-A,B,C mRNA than
10 to induced E-mRNA or C56 mRNA (Wallach et al. (1982)); on the other
hand, some subspecies of interferon-alpha, such as alpha-d can induce
E-mRNA when a concentration 100 times lower than those needed to
induce HLA-A,B,C mRNA. A comparison of the hybridization of differ-
ent cloned cDNAs to the same RNA sample, can indicate what type of
15 interferon is involved. Thus, more information can be derived from
the comparison of different cDNA than from the use of only one cDNA
probe.

EXAMPLE 3

20

A KIT FOR THE MEASURE OF INTERFERON-INDUCED mRNAs

The Kit would provide the cloned cDNA specific for the mRNA of the
(2'-5') oligo A synthetase and for the mRNA of the 56,000 Mr protein,
25 described herein, as well as reagents to carry out the hybridization
tests: comprising reagents for nick-translation with deoxy-ribonuc-
lease I and (³²P)-gamma-dCTP, reagents for hybridization on nitrocell-
ulose membranes, and reagents for RNA extraction from the cells.

EXAMPLE 4

30

SEQUENCE OF cDNA FOR THE 1.6 KB (2'-5') OLIGO A SYNTHETASE mRNA

The partial E1 cDNA clone (Merlin et al, 1983), shown to be the 3'
end of the 1.6 kb (2'-5') oligo A synthetase by IFN in human cells
(Benech et al, 1985) was used to screen a lambda gt10 cDNA library
35 from SV80 cell RNA (Wolf and Rotter, 1985). By restriction mapping,
clone lambda gt10 9-2 was found to contain the E1 cDNA at the 3'
end of a 1.32 kb EcoR1 insert (Fig. 6A) which was subcloned in pBR
(9-21 cDNA). Sequencing was carried out as outlined in Fig. 6A

1 and confirmed that the 9-21 cDNA contains the C-terminus and 3'-un-
 translated sequence previously reported for the E1 cDNA (Merlin et al,
 1983). The 9-21 cDNA sequence (Fig. 7) predicts an open reading
 frame of 364 aminoacids starting at an ATGATG sequence. A computer
 5 program based on the 3-base periodicity of protein-coding sequen-
 ces (Trifonov, 1984) indicated that the only compatible reading
 frame is the one starting from this ATGATG. It is possible that
 translation initiates at the second ATG in this site, since it is
 the only one preceded by an A at -3 and having homology with the
 10 consensus translation initiation sequence (Kozak, 1984).

The enzyme thus coded by the 1.6 kb (2'-5') oligo A synthetase RNA
 would have a molecular weight of 41,700, in good agreement with the
 apparent 38,000-Mr protein seen by SDS-polyacrylamide gel electro-
 15 phoresis of the in vitro translation product of RNA hybridized to
 E1 cDNA (Merlin et al, 1983). The C-terminal heptadecapeptide pre-
 dicted by the open reading frame, was synthesized chemically and
 used to immunize rabbits. The antiserum obtained (C in Fig.12)
 precipitates specifically a protein migrating at 38,000-Mr in SDS
 20 gel electrophoresis from 35S-methionine labeled extracts of cells
 treated by IFN which is absent from untreated cells. Two experiments
 confirmed that this protein has (2'-5') oligo A synthetase activity:
 it was removed from the extracts by passage through a poly (rI)(rC)
 agarose column, and the supernatant remaining after immunoprecipi-
 25 tation was depleted of a large part of the enzymatic activity.

EXAMPLE 5

SEQUENCE OF cDNA FOR THE 1.8 KB (2'-5') OLIGO A SYNTHETASE mRNA

A genomic DNA fragment corresponding to the additional exon of the
 30 1.8 kb RNA (Benéch et al, 1985; see Fig. 9) was used as probe to
 isolate a E18 cDNA clone, 48-1, from the same lambda gt10 cDNA li-
 brary of SV80 RNA. The restriction map of the E18 cDNA clone (Fig.
 6B) confirmed that its 5' end is part of the E16 cDNA but that its
 3' end differs. Sequencing (Fig. 7) revealed that the junction
 35 is at nucleotide 1071 of the E16 9-21 cDNA clone, the last 247
 nucleotide of E16 being replaced by a 515 nucleotide-long se-
 quence terminated by a different polyadenylation site. This diffe-
 rence accounts for the 0.2 kb difference in size between the two

1 mRNAs seen on Northern blots. The 5' portion of the E18 cDNA shows
no base change from the sequence of the E16 cDNA, but is incomplete.
The gene mapping described below, indicates that both 1.6 and 1.8
kb mRNAs have the same 5' end.

5 The 3' region of the E18 cDNA which diverges from the E16 sequence,
contains an open reading frame ending after 54 codons. This rea-
ding frame, which leaves a 350 nucleotides-long untranslated
region, was confirmed by the computer program based on the 3 base
10 periodicity of protein-coding sequences (Trifonov, 1984). An al-
ternate longer open reading frame would not be in the same com-
puted phrase as the 5' portion common with the E16 cDNA. A hydro-
pathy plot (Kyte and Doolittle, 1982) on the predicted C-termini
of the 1.6 and 1.8 kb mRNA protein products, indicates a striking
15 difference between the two forms of the (2'-5') oligo A synthetase
(Fig. 8). The C-terminus of the E16 protein is very hydrophobic,
while that of the E18 protein is hydrophilic and contains two
acidic regions (Asp-Asp-Glu-Thr-Asp-Asp and Glu-Glu-Asp) (Fig. 7).
Futhermore, a possible glycosylation site is present in the C-ter-
minus of the E18 product (Fig. 7).
20

The 9-21 cDNA was subcloned in λ gt11 so as to fuse the coding
frame in phase with the lac Z gene. Extracts of the E.coli lysogen
containing this phase, showed clearly (2'-5') oligo A synthetase
25 activity after binding to poly(rI)(rC) agarose, while no activity
was found when the 9-21 cDNA has been fused in the opposite orien-
tation (Fig.13). This expression in E.coli demonstrates that the
cDNA indeed corresponds to the structural gene coding for the ds
RNA activated (2'-5') oligo A synthetase and that the protein
30 of about 40 kd coded by the IFN induced RNA is the enzyme itself,
and not a regulatory factor. This protein does not seem to require
post-translational modifications to exhibit enzymatic activity.

The transformed cell containing the 9-21 cDNA has been designated
35 Escherichia coli lambda-gt11-E16 and deposited under Accession No.
I496 with the Collection National Cultures de Micro-organismes,
Institut Pasteur, 25 rue du Docteur Roux, 75724-Paris-Cedex 15,
France. This deposit was made pursuant to the Budapest Treaty On the

- 1 International Recognition Of The Deposit Of Microorganisms For The
Purposes Of Patent Procedure.

EXAMPLE 6

ORGANISATION OF THE HUMAN (2'-5') OLIGO A SYNTHETASE GENE

5

Three overlapping genomic clones were isolated using the E1 cDNA
as probe (Benec'h et al, 1985), one from a library of partial EcoR1
digest of human blood cell DNA (Mory et al, 1981) and two from a
library of partial Alu1 and Hae3 digest of embryonic human DNA
10 (Maniatis et al, 1978). The genomic clones represent about 29 kb
of human DNA and no evidence for more than one E gene was found
while screening the libraries. Southern blots of genomic DNA are
consistent with the existence of a single gene (Fig. 9). By Nor-
thern blot analysis using genomic DNA fragments as probes, by S1
15 nuclease mapping and by sequencing, the E16 cDNA 9-21 was shown
to correspond to five exons on the gene (Fig. 9). The ATGATG se-
quence is found in exon 3, while the termination codon and 3'
untranslated region with the polyadenylation site of the 1.6 kb
RNA are found in exon 7. The structure of the more 5' exons 1 and
20 2 is described below. The sequences of the intron-exon boundaries
were determined (Table 2) and follow the CAG and GT rule for the
splice acceptor and donor sites (Breathnach and Chambon, 1981).

A sequence CTGAC/T is commonly found not far from the splice
acceptor, as reviewed recently by Keller (1984). It is notable
25 that the CTGAC/T region shows base complementarity to the se-
quence of the intron/exon 3' boundary (acceptor site; Table 2),
in addition to the complementarity of the intron donor site with
the CTGAC sequence pointed out by Keller (1984) as playing a role
in the lariat model.

30

The sequences of the 5 exons containing the coding region of the
(2'-5') oligo A synthetase produced by the 1.6 kb mRNA, would in-
dicate that the enzyme is composed of domains with differing amino-
acid compositions (Table 3). The first exonic domain (60 amino acids)
35 is rich in aspartic acid, in the second (aminoacids 61 to 156) ar-
ginine is predominant, the two next exons (aminoacids 157 to 218
and 219 to 295) are lysine rich, and the C-terminus of the E16
product (296 to 364) is very rich in proline and alanine.

1

TABLE 2

EXON-INTRON BOUNDARIES IN THE HUMAN (2'-5') OLIGO A SYNTHETASE GENE

5	<p>(4.2):-50 <u>..CCCTTCTGAGGAAACGAAACCAACAG:CAGTCCAAG....</u> exon 3 ..AAG.GTG.GTA.AAG:GTGAGCGG.... 1.3 kb 213</p>
10	<p>(4.2)..GGTTGGCTTACTAAG:214 CATCAATTATTATTTTGTCTTTTTCAG:GGT.GGC.TCC.TCA.. exon 4 ..GAT.GCC.CTG.G:GTGAGAGCTC... 2.3 kb 502</p>
15	<p>(3.3)..GAAGAGCTGAC:503 CCTAAGTGTGAAGTTTACCCACACAG:GT.CAG.TTG.ACT.. exon 5 ..TGG.TAC.CAA.AAT:GTATGGTTT.... 5.3 kb 687</p>
20	<p>(3.1)..TGAGCAAACCA:688 <u>TTTTTTCTGATTGTTTTCTCTTCTCAG:TGT.AAG.AAG.AAG..</u> exon 6 ..ACG.AAA.CCC.AG:GTATGCTATCCACATGGCTTG.. 0.9kb 916</p>
25	<p>(3.1) -Pst 1:-917 <u>TACCTGTCTCTCTAAATGCTGCTCTGCAG:G.CCT.GTG.ATC...</u> exon 7a ..TGG.ATT.CTG.CTG:GTGAGACCT....GAATTCATTCCTTAAG 1071:AGTAATAATAATAATCTCTAACACCAATT ATTCACTGTCTGCTTCGGGCTC.. 1.4kb (whole intron = 1.6 kb)</p>
30	<p>(6.8) BamH1- GGATCCAG: ATGGCATGTCACAGTATACTAAATGCTCAG: T ATCCAGCTGCAATGCAGGAAGACTCC:1072 exon 8 (1.2 kb RNA) 1585 CTGATGTGATCATGTGTCTACCCCTTCAG:GCT.GAA.AGC...AATAAAATAAGCAAATACCAATTATGGGTC..</p>

For exon numbering see Fig. 7 and 9. The self-complementary regions between the CTGAT/C, or CITAC, CTGTC (Keller, 1984) and splice acceptor CAG are underlined. The polyadenylation sites with a conserved undecanucleotide of the 1.6 and 1.8 kb RNAs (see Fig. 7) are underscored by dots. The numbers in parentheses are the size of the Eco RI genomic fragments carrying the introns or exons (see Fig. 9). The start and end of each exon is numbered as in the 9-21 E cDNA of Fig. 7.

35

TABLE 3

EXONIC DOMAINS OF THE E16 AND E18 (2'-5') OLIGO A SYNTHETASES

AA	E16 C-term. E18 C-term.						
	1-60 (60)	61-156 (96)	157-218 (62)	219-295 (77)	296-346 (51)	347-364 (18)	347-400 (54)
ALA	2 (3.3)	7 (7.3)	0 (0.0)	3 (3.9)	4 (7.8)	3 (16.7)	4 (7.4)
ARG	4 (6.7)	10 (10.4)	3 (4.8)	5 (6.5)	1 (2.0)	1 (5.6)	2 (3.7)
ASN	1 (1.7)	2 (2.1)	2 (3.2)	3 (3.9)	3 (5.9)	0 (0.0)	1 (1.9)
ASP	6 (10.0)	5 (5.2)	2 (3.2)	1 (1.3)	4 (7.8)	0 (0.0)	5 (9.3)
CYS	4 (6.7)	1 (1.0)	2 (3.2)	2 (2.6)	1 (2.0)	0 (0.0)	1 (1.9)
GLN	1 (1.7)	7 (7.3)	6 (9.7)	5 (6.5)	2 (3.9)	0 (0.0)	3 (5.6)
GLU	2 (3.3)	7 (7.3)	5 (8.1)	4 (5.2)	2 (3.9)	1 (5.6)	5 (9.3)
GLY	2 (3.3)	9 (9.4)	3 (4.8)	3 (3.9)	6 (11.8)	0 (0.0)	2 (3.7)
HIS	1 (1.7)	0 (0.0)	1 (1.6)	1 (1.3)	0 (0.0)	1 (5.6)	3 (5.6)
ILE	5 (8.3)	2 (2.1)	3 (4.8)	4 (5.2)	2 (3.9)	1 (5.6)	2 (3.7)
LEU	5 (8.3)	13 (13.5)	8 (12.9)	10 (13.0)	6 (11.8)	2 (11.1)	2 (3.7)
LYS	5 (8.3)	2 (2.1)	7 (11.3)	9 (11.7)	2 (3.9)	0 (0.0)	1 (1.9)
MET	3 (5.0)	0 (0.0)	0 (0.0)	1 (1.3)	0 (0.0)	0 (0.0)	0 (0.0)
PHE	4 (6.7)	7 (7.3)	3 (4.8)	3 (3.9)	1 (2.0)	1 (5.6)	1 (1.9)
PRO	3 (5.0)	4 (4.2)	3 (4.8)	4 (5.2)	6 (11.8)	5 (27.8)	4 (7.4)
SEP	4 (6.7)	8 (8.3)	3 (4.8)	1 (1.3)	3 (5.9)	2 (11.1)	5 (9.3)
THR	2 (3.3)	4 (4.2)	5 (8.1)	6 (7.8)	1 (2.0)	0 (0.0)	8 (14.8)
TRP	0 (0.0)	1 (1.0)	1 (1.6)	2 (2.6)	4 (7.8)	0 (0.0)	1 (1.9)
TYR	2 (3.3)	0 (0.0)	3 (4.8)	7 (9.1)	1 (2.0)	0 (0.0)	4 (7.4)
VAL	4 (6.7)	7 (7.3)	2 (3.2)	3 (3.9)	2 (3.9)	1 (5.6)	0 (0.0)

Although the E18 cDNA 48-1 is incomplete, we found that exons 1-6 (Fig. 9) hybridize to the 1.8 kb mRNA as well as to the 1.6 kb mRNA on Northern blots. The structure of the two RNAs is most likely identical up to exon 7. The additional splicing from the middle of exon 7 to exon 8 characterizing the E18 cDNA, was confirmed by sequencing these intron-exon boundaries in the genomic DNA clone (Table 2). The truncated exon 7a present in the E18 cDNA is followed by a 1.6 kb intron containing the polyadenylation site of the 1.6 kb RNA. Exon 8 begins 98 bp downstream from the unique BamH1 site of the gene (Table 2, Fig. 9). The genomic exon 8 ends by the polyadenylation site of the 1.8 kb RNA, characterized by a tandem repeat of the AATAAA signal. Although exon 7 and 8 have no homology, a conserved undecanucleotide ACCATTTATTG, in which the third cytidine is polyadenylated, is present at the end of both exons (Table 2). As pointed out previously (Benecch et al, 1985), a hairpin-loop structure can be formed in both cases between this conserved undecanucleotide and the AATAAA region; such structures may participate in the cell-specific mechanism which determines whether cleavage and polyadenylation of the transcripts occur

1 at the end of exon 7 or at the end of exon 8.

Based on the above gene mapping, the enzyme coded for by the 1.8 kb mRNA should be identical to the E16 product in the first 346 amino-
 5 acids, which are followed by a specific 54 aminoacid-long region, rich in aspartic, glutamic acid and threonine. The 400 aminoacid-long E 18 enzyme would have a molecular weight of 46,000. -

EXAMPLE 7

10

TWO FORMS OF THE HUMAN (2'-5') OLIGO A SYNTHETASE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE

Northern blot analysis of SV80 RNAs revealed that 3 species of RNA
 15 (1.6, 1.8 and 3.6 kb) hybridizing to E1 cDNA accumulate in cells up to 12 hours after exposure to IFN (Merlin et al, 1983). Additional unstable transcripts were also seen. The relationship between these RNAs was investigated by transcript mapping on genomic DNA clones. In two human genomic libraries, the E1 cDNA identified
 20 only one series of overlapping genomic DNA clones which represent 29 kb of human DNA (Fig. 9A) and were found to contain an apparently unique (2'-5') oligo A synthetase gene (Benecch et al, 1985a). By S1 nuclease analysis and partial gene sequencing, the 9-21 (E1) cDNA was found to correspond to 5 exons (numbered 3-7
 25 on Fig. 9A and in the sequence of Fig.7). The 3' end and polyadenylation site of this cDNA was indentified at the end of exon 7 (Fig. 9). However, hybridization of further downstream genomic DNA fragments to Northern blots of SV80 RNA, revealed (Benecch et al, 1985) that only the 1.6 kb RNA ended at the polyadenylation site
 30 in exon 7, while both the 1.8 and 3.6 kb RNAs hybridized to an additional exon located 1.6 kb downstream and which ends also by a polyadenylation site (exon 8, Fig. 9). Thus the 9-21 (E1) cDNA represents the 1.6 kb RNA and was renamed E16 cDNA. It was further found that the 3' half of exon 7 does not hybridize to the 1.8 kb
 35 RNA indicating that the transcript is formed by a splicing event from the middle of exon 7 to exon 8. All the 5' upstream exons hybridized to both 1.6 and 1.8 kb RNAs, indicating that the 2 RNAs differ only in their 3' ends. This was confirmed by the isolation

- 1 from the SV80 λ gt10 cDNA library of a cDNA clone for the 1.8 kb
RNA (clone 48-1 or E18 cDNA, Fig. 7B), which demonstra-
ted the differential splicing and ended at the polyadenylation
site of exon 8 (Fig. 4). A similar cDNA clone was found in a Daudi
5 cDNA library by Saunders and Williams (1984). The E18 sequence
locks the last 247 nucleotides of E16 which are replaced by 515 nu-
cleotides accounting for the difference in size between the 1.6
and 1.8 kb RNAs.
- 10 The 1.8 kb RNA would thus code for a 46,000-Mr protein (E18) which
differs from the E16 protein in its C-terminus. Like the E16 pro-
tein, the E18 product has ds RNA binding and (2'-5') oligo A
synthetase activity as shown by translation of mRNA selected by
hybridization to E18-specific DNA fragments (Benech et al, 1985).
- 15 This suggests that the first 346 aminoacids common to the 2
proteins contain the catalytic sites. Examining the exon composi-
tion this common part appears composed of a N-terminal acidic domain,
followed by three basic regions. The last 18 residues of the E16
protein form a very hydrophobic domain, which is replaced in E18
20 by a longer hydrophilic and acidic region which also contains a
potential glycosylation site. This difference between the 2 en-
zymes may determine their ability to dimerize, or interact with
other proteins and cellular structures. For example, E16 may bind
to membranes while E18 may interact with basic proteins in ribo-
25 somes or in the nucleus.

Two forms of the (2'-5') oligo A synthetase were found by gel fil-
tration in extracts of IFN-treated human cells (Revel et al, 1982):
a 30-40 Kd enzyme which could correspond to a monomeric form of
30 the E16 or E18 proteins, and a 60-80 Kd enzyme which remains to
be identified. The 3.6 kb RNA does not seem to code for a large
enzyme since transcript mapping showed that this RNA contains
intronic regions (e.g. between exon 7 and 8) which are removed
from the 1.8 kb RNA and have no open reading frame. We also failed
35 to see large E mRNA in oocyte translations. A 80 Kd protein in
SDS was reported in purified human (HeLa) synthetase (Yand et al,
1981) but its enzymatic activity was not demonstrated. In enzyme
purified from Namalva and CML cells (Revel et al, 1981b) we could

-30-

- 1 detect a 40 Kd band in SDS. Thus it remains possible that the 60-
80 Kd enzyme form is a dimer of the 40 Kd protein. The human
synthetase may differ from that in mouse cells where a large 3.8
kb RNA was seen under denaturing conditions which codes for a 80
5 Kd enzyme (mainly cytoplasmic), in addition to a 1.5 kb RNA coding
for a 30 Kd enzyme (mainly nuclear) (St. Laurent et al, 1983).
The human E cDNA detects a 3,8-4 kb and a 1.6-1.7 kb RNA in mouse
cells, the large RNA hybridizing to E18-specific DNA (Mallucci et
al, 1985). It is possible that in human cells the large RNA is
10 further processed into 1.8 kb RNA, which has not been seen in mouse
cells. Shulman et al (1984) have used the fact that the bulk of the
(2'-5') oligo A synthetase in human cells behaves as a smaller pro-
tein than in mouse cells to map the human synthetase gene to chro-
mosome 11 in human rodent-hybrid cells. Antisera specific to E16
15 and E18 will help to elucidate the relationship between these pro-
teins and the two forms of the native enzyme seen in human cells.

EXAMPLE 8

20 CELL-SPECIFIC EXPRESSION OF THE TWO (2'-5') OLIGO A SYNTHETASE mRNAs

- RNA from a number of human cell lines have been examined in Northern
blots with the E cDNA probes (Merlin et al, 1983; Benech et al,
25 1985). Table 4 shows that human cells can be grouped in 3 classes
according to the predominant E mRNA species induced by IFN. Lympho-
blastoid B cell lines from Burkitt lymphomas have mainly the 1.8
kb RNA. Instead, several cell lines have the 1.6 and 3.6 kb RNA
but little 1.8 kb RNA. If the 3.6 kb RNA is a partially spliced
30 precursor of the 1.8 kb RNA, these cells may have an inhibition
in the processing of the 3.6 kb RNA. T-lymphocyte lines (CEMT from
an acute leukemia and Gash from hairy cell leukemia) contain like
fibroblastic cells, all 3 E RNA species. The E18 polyadenylation
(pA) site seems, therefore, to be used in all human cells to
35 produce either 3.6 or 1.8 kb RNA. The E16 pA site seems not to be
used in B lymphoblastoid cells. A conserved undecanucleotide pre-
sent in both E16 and E18 pA sites (Fig. 9B) can form a hairpin-
loop with the AATAAA signal and could have a role in site selec-

- 1 tion (Benecch et al, 1985). E18 has a tandem repeat of the AATAAA
 signal (Fig. 9B) and could be a stronger pA site. Transcripts en-
 ding at the E18 pA site accumulate earlier after IFN addition than
 the 1.6 kb RNA (Benecch et al, 1985).

5

TABLE 4

PREDOMINANT (2'-5') OLIGO A SYNTHETASE RNA SPECIES

10

	3.6 kb		3.6 kb
		1.8 kb	1.8 kb
	1.6 kb		1.6 kb
15	Histiocytic lymphoma U937	B lymphoblastoid Burkitt lymphoma: - Daudi - Namalva - Raji	Fibroblastic: -SV80 -FS11
	Amniotic Wish Cervix Ca HeLa Raji x HeLa hybrids		T cells: -CEMT Hairy cell-leuk.: -Gash
20			

25

The type of synthetase predominantly made may vary in different
 human cells. We found no correlation between the cytoplasmic or
 nuclear localization of the synthetase and the type of RNA pre-
 sent in the cells. However, Namalava cells seemed to have mainly
 the 30-40 Kd enzyme upon gel filtration while HeLa and SV80 cells
 had also the 60-80 Kd form (Revel et al, 1982).

30

EXAMPLE 9PROMOTER REGION OF THE (2'-5') OLIGO A SYNTHETASE GENE

35

The SphI-SphI fragment of 0.85 kb (Fig.10) from the genomic 4.2 kb
EcoR1 fragment (Fig. 9) which contains part of exon 3 of the E16
 cDNA 9-21 clone, hybridized in Northern blots with the 1.6, 1.8,
 2.7 and 3.6 kb RNAs. However, upstream regions did not. Several

-32-

1 experiments allowed to localize the RNA transcriptional start in
its fragment. S1 nuclease analysis first showed that exon 3 starts
about 50 nucleotides upstream of the end of the 9-21 cDNA. A
primer extension experiment using an oligonucleotide from the end
5 of the 9-21 cDNA, indicated that the 5' end of the mRNA is about
230 nucleotides from the 5' end of this cDNA. RNA hybridization
with riboprobes produced in SP6 (Green et al, 1983) and RNase
digestion indicated two exons of 70 and 110 nucleotides preceding
exon 3. By S1 nuclease analysis using a probe labeled at the
10 unique Hpa1 site (Fig. 9), the 5' end of the mRNA was finally
located 17 nucleotides upstream from the Hpa1 site. The sequence
of this region is shown in Fig. 6. The location of the transcrip-
tion initiation site 17 residues before the Hpa1 site, is suppor-
ted by the presence of a TATAA box at position -30. A striking
15 feature of the upstream sequences, is the high purine content
(69.6%) mostly adenine (58.9%). Run of a homology materix with
other known promoter upstream sequences, revealed a surprising
homology with the human IFN promoters, in particular with the
sequence of the IFN- β 1 gene promoter (Degrove et al, 1981). The
20 purine-rich region from -75 to -85 of the IFN- β 1 promoter, which
contains the essential transcription signal described by Zinn
et al (1983), shows 90% homology with the region of the presumed
promoter of the (2'-5') oligo A synthetase just upstream of the
TATAA box (-40 to -50) (Fig. 11). This purine-rich signal is repea-
25 ted in the IFN- β 1 promoter in the segment between the TATAA box
and the cap site; in this region, which may also have regulatory
functions (Nir et al, 1984) the homology between the IFN- β 1 gene
and the (2'-5') oligo A synthetase gene is high. In contrast, search
for homology with promoters of other genes, such as HLA genes
30 (Malissen et al, 1982; Schamboeck et al, 1983) and the metallo-
thionein II gene (Karin and Richards, 1982) which are activated
by IFNs (Fellous et al, 1982; Rosa et al, 1983b; Friedman et al,
1984) showed no apparent sequence relationship in this region of
the (2'-5') oligo A synthetase gene promoter. No significant ho-
35 mology was also seen with the body of the IFN- β 1 gene.

The 5' untranslated leader of the (2'-5') oligo A synthetase mRNA
(exon 1, 2 and part of exon 3) contains two short introns whose

- 1 position was tentatively determined by S1 analysis as shown in Fig.
6. The entire human (2'-5') oligo A synthetase gene is about 13
kb (Fig. 9) and the sum of the exons agrees with the observed sizes
of the mRNAs.

5

EXAMPLE 10

LAMBDA GT10 cDNA CLONES OF THE (2'-5') OLIGO A SYNTHETASE

- 10 A λ gt10 cDNA library prepared from poly A+ RNA of human SV80 cells
(Wolf and Rotter, 1985) was screened using as probe the Pst1-Pst1
insert of the E1 cDNA plasmid described previously (Merlin et al,
1983). The insert corresponding to the 3' end of the 1.6 kb E RNA
(Benech et al, 1985), was purified by agarose gel electrophoresis
15 and nick-translated (Rigby et al, 1977). Plaques were repeatedly
picked from 9cm plates (10^5 phages), and small scale λ DNA pre-
parations were analyzed by restriction mapping by routine procedures
(Maniatis et al, 1982). Fifteen λ gt10 cDNA clones containing the
E1 cDNA fragment were isolated and phages 9-2 and 5-2 with the lon-
20 gest inserts were cut by EcoR1 and the inserts subcloned in
pBR322 to obtain E16 cDNA clones 9-21 and 5-21 of Fig. 1A. The
same library was rescreened with a human genomic Pst1-Pst1 0.9 kb
fragment from phage λ chE1 (Benech et al, 1985), a fragment which
specifically hybridizes to the 1.8 kb RNA. We thereby isolated
25 λ gt10 cDNA clone 48-1 of Fig. 1B, along with another cDNA clone
representing a partially spliced E RNA. Sequencing was carried out
according to Maxam and Gilbert (1980). Restriction enzymes were
from New England Biolabs and Boehringer. Homology matrix and hy-
dropathy plot computer programs of Pustell and Kafatos (1982a,b)
30 were run on IBM PC. Three base periodicity to locate protein co-
ding frames was computed according to Trifonov (1984).

EXAMPLE 11

GENOMIC DNA CLONES CONTAINING THE (2'-5') OLIGO A SYNTHETASE GENE

35 Three overlapping genomic clones were isolated as previously
described (Benech et al, 1985): λ chE1 from a partial EcoR1-cut

-34-

1 DNA library (Mory et al, 1981) and λ chE2 and E3 from a partial
 Alu1/Hae 3 DNA library (Maniatis et al, 1978). The genomic EcoR1
 fragments of these phages were subcloned in pBR322. Exon mapping
 was done 1) by Southern blot hybridization of restriction digests
 5 from subcloned genomic fragments to various cDNA probes, 2) by
 hybridization of genomic DNA restriction fragments to Northern
 blots of poly A+ RNA from IFN-treated and untreated cells as
 described (Benech et al, 1985) and 3) by sequencing of intron-exon
 boundaries in comparison to cDNA.

10

The internal Sph1-Sph1 0.87 kb segment of the genomic 4.2 kb EcoR1
 fragment containing the 5' end of the mRNA, was subcloned in the
 Sph1 site of pBR322 before sequencing. Primer extensions using
 synthetic oligodeoxyribonucleotides of 18-20 bases complementary
 15 to the mRNA (gift of Dr. D. Segev, InterYeda) were done as before
 (Rosa et al, 1983a). Riboprobes synthesis after subcloning in the
 SP6 vector were carried out according to instructions of Promega
 Biotec. DNA from Daudi lymphoblastoid cells and from FS11 foreskin
 fibroblasts was prepared according to Wigler et al (1979) and
 20 Southern blot analysis was done on Gene-Screen Plus nylon fiber
 sheets using hybridization procedure B recommended by the manu-
 facturer (New England Nuclear).

EXAMPLE 12

25

QUICK CELL BLOT ASSAY OF (2'-5') OLIGO A SYNTHETASE RNAs FOR THE CLINICAL MONITORING OF IFN ACTION

The usefulness of measuring the (2'-5') oligo A synthetase has been
 30 shown in human peripheral blood mononuclear cells (PBMC) to
 monitor the response of patients to IFN- β (Schattner et al, 1981a)
 and IFN- β i.m. injections (Schoenfeld et al, 1984). Since the en-
 zyme level of PBMC in normal individuals is rather constant, this
 assay has allowed to diagnose viral infections evidence by an in-
 35 crease in the enzyme in the PBMC and granulocytes (Schattner et al,
 1981b, 1984; Schoenfeld et al, 1985). Decrease in the enzyme cha-
 racterize acute leukemias with numerous blust cells (Wallach et al,
 1982; Schattner et al, 1982). This technique has also been pioneered

1 by Williams et al (1981) and is now in wide use.

Synthetase E is strongly induced in cells treated by all three types of IFNs, alpha, beta and gamma, and its increase is a good marker of
5 IFN activity (Wallach et al., 1982). It is therefore possible to use measurements of E levels to determine whether cells in vitro or in vivo have been exposed to IFN and respond to it. This measurement may be used as an assay for IFN in unknown solutions, by exposing cells to said solutions and determining the increase in E levels
10 (Revel et al., U.S. Patent No. 4,302,533). The measurement may also be used to establish whether IFN is produced in increased amounts in whole organisms including man.

The (2'-5') oligo A synthetase increases during differentiation of
15 hematopoietic cells as a result of autocrine secretion of IFN-beta (Yarden et al., 1984). Another important application of E measurements is in the monitoring of patients under IFN therapy. Besides clinical changes, it is possible to establish that the patients respond to IFN by measuring the PMBC E level which increases 5-10 fold
20 during systemic IFN-alpha as well as beta treatment (Schattner et al., 1981a; Schoenfeld et al., 1984). It is clear that assay of other IFN-induced activities or molecules may be used as well as the assay of the E enzyme, but this method has been the most widely used (Williams et al., Borden).

25 Now the assay of E RNA in human PMBC is used for the same purpose. A quick cell blot (Cheley and Anderson, 1984) using the 9-21 E cDNA as probe was developed for PMBC (Fig. 14). Oligonucleotides derived from the E cDNA may also be used as probes. The effect of 10 U/ml
30 IFN can easily be detected by this method (Fig. 15). Positive signals were obtained in a patient treated by 10^7 units/day of IFN-alpha-c.

EXAMPLE 13

35

OBTENTION OF ANTIBODIES TO (2'-5') OLIGO A SYNTHETASE

Two peptide sequences were chosen from the total aminoacid sequences

-36-

- 1 of E16 and E18, to serve as antigens for the induction of antibodies against the native (2'-5') oligo A synthetase activity molecule.

Peptide B:

GLU LYS TYR LEU ARG ARG GLN LEU THR LYS PRO ARG PRO VAL ILE LEU ASP

- 5 PRO ALA ASP

comprises aminoacids 284 to 303 common to both E18 and E16 sequences.

Peptide C:

ARG PRO PRO ALA SER SER LEU PRO PHE ILE PRO ALA PRO LEU HIS GLU ALA

comprises the C terminus of E16 (residues 348 to 364). Both peptides

- 10 were synthesized by the solid-phase peptide synthesis method of Barany and Merrifield (1980). After purification on Sephadex G25 columns in 2M acetic acid, the peptides were linked to Keyhole Limpet Hemocyanin (Calbiochem). Esterification of the NH₂-terminal arginine of peptide C with p-aminophenylacetic acid allowed to covalently link the peptide to the carrier protein through its amino-
- 15 terminus (Spirer et al, 1977). Peptide B was coupled to the carrier protein by ethylene diamine carbodiimide (Hoare and Koshland, 1967).

- Rabbits were injected subcutaneously with 1 mg carrier-coupled
- 20 peptide (equivalent to 0.2 mg pure peptide) which was emulsified in complete Freund's adjuvant. Rabbits were boosted twice at two weeks intervals with 0.5 mg of carrier-coupled peptide in incomplete adjuvant, and were continued until maximal antibody response. The titer of antibodies in the rabbit sera were measured in enzyme-linked imm-
- 25 unosorbent assays (Green et al, 1982) using the carrier-free peptides.

EXAMPLE 14

- 30 USE OF ANTI-(2'-5') OLIGO A SYNTHETASE ACTIVITY PEPTIDE ANTIBODIES TO DETECT THE ENZYME

Extracts of IFN-treated human cell cultures

- 35 The fibroblastoid cell line SV80 and the amniotic cell line Wish were grown to confluent monolayers on plastic dishes and the Daudi cell line was grown in suspension to 1.5×10^6 cells/ml. Cultures were treated for 16-24 hours with rIFN- β 1, 500 U/ml. The human rIFN- β 1

-37-

- 1 was produced by genetically engineered CHO cells and purified to homogeneity by monoclonal antibody affinity chromatography (Chernajovsky et al, 1984).
- 5 Cells were washed twice with phosphate buffered saline (PBS) at 4°C and lysed in the cold in Buffer A: 20mM Hepes buffer, pH 7.5, 5mM Mg acetate, 30 mM β -mercaptoethanol, 100 μ M phenylmethyl sulfonyl fluoride (PMSF), 10% glycerol and 0.5% Nonidet P-40 (NP40). Nuclei and unbroken cells were eliminated by centrifugation at 1,500 γ for
- 10 10 min. The supernatant (S1.5) was centrifuged 10 min at 15,000 γ in an Eppendorf Microfuge to obtain mitochondria and lysosomes-free supernatant (S15). Protein concentrations were measured by Micro-assays (Bradford, 1976).
- 15 Centrifugation of S15 for 2 hours at 100,000 γ in a Beckman refrigerated ultracentrifuge was used to prepare cell sap (S100) and microsomes (P100) fractions.

EXAMPLE 15

20

ASSAY OF THE (2'-5') OLIGO A SYNTHETASE

- Aliquots of S15 containing 1-2 μ g protein were incubated in 20 μ l reactions containing 25mM Hepes buffer, pH 7.5, 20mM Mg acetate, 1mM
- 25 dithiothreitol, 1.5mM ATP, 4 μ Ci of 32 P- α -ATP, 50 μ g/ml poly(rI)(rC) (from PL-Biochemicals) for 2 hours at 30°C. After boiling for 5 min and Microfuge centrifugation, Bacterial Alkaline Phosphatase was added at 25 U/ml to an aliquot and the reaction incubated for 2 hours
- 30 at 37°C. From 2 to 7 μ l were spotted on Whatmann 3MM paper and analyzed by electrophoresis at 3,000 V in pyridine/acetic acid pH 3.5. After autoradiography, the (A2'p)nA oligomers spots were cut out and counted.

EXAMPLE 16

35

ELECTROPHORETIC-TRANSFER IMMUNOBLOTS

Aliquots of crude cellular fractions (30 μ g protein) were adjusted

-38-

1 with Laemmli's sodium-dodecyl-sulphate-polyacrylamide gel electro-
 phoresis loading buffer (Laemmli, 1970) and boiled 10 min before
 electrophoresis on 7.5 or 10 % gels. Amersham's ^{14}C -methylated
 proteins were used as molecular weight standards (10^4 cpm). Electro-
 5 phoretic transfer onto nitrocellulose paper (Schleicher and Schull
 BA85) was carried out in 25 mM Tris-base, 192mM glycine and 20% meth-
 anol. The blots were preincubated in 0.09M NaCl, 0.01M Tris-HCl pH
 7.5, 10% (v/v) of a 1% fat milk solution, 10% (v/v) heat-inactivated
 fetal calf serum and 0.05% Tween-20, either for 2 hours at 37°C or
 10 overnight at 4°C followed by 30 min at 37°C. Blots were then incub-
 ated with anti-(2'-5') oligo A synthetase peptide B antibod-
 ies in form of rabbit IgG 0.1mg/ml, for 2 hours at 37°C. Blots were
 washed 5 times for 10 min in 4% fetal calf serum and incubated in the
 complete above preincubation mixture containing 10^6 cpm/ml of ^{125}I -
 15 protein A (Amersham, 30 mCi/mg) for 1 hour at 37°C Blots were washed
 and subjected to autoradiography.

EXAMPLE 17

20 IMMUNOPRECIPITATION OF (2'-5') OLIGO A SYNTHETASE ACTIVITY AND LABELED PROTEINS

First aliquots of 5-10 μ l anti-(2'-5') oligo A synthetase
 peptide B rabbit serum were adsorbed on 3mg of Protein A-Sepharose
 25 (Pharmacia) equilibrated in PBS with 3% Bovine serum albumin (BSA),
 for 30 min at room temperature, then washed with PBS-1% BSA. For
 immunoprecipitation of the (2'-5') oligo A synthetase enzymatic
 activity, aliquots of 2 μ g of S15 proteins in a final volume of 20 μ l
 of buffer A were adsorbed on the above pelleted IgG-Protein A
 30 Sepharose for 2 hours at 4°C. The suspension was diluted 5 fold in
 buffer A and the supernatant transferred to another tube. The pellet
 was washed 3 times with 0.5 ml buffer A and was then suspended in
 25 μ l of the enzyme reaction mixture (see above). Activity was
 measured also on aliquots of the non-bound supernatant.

35

For labeling (2'-5') oligo A synthetase, Wish cells were
 grown to confluent monolayers on 3cm plastic dishes and treated for
 12 hours with 500 U/ml rIFN- β 1. The medium was replaced by 0.5 ml

-39-

- 1 methionine-free DMEM (GIBCO) containing 500 μ Ci of 35 S-methionine (Amersham 400 mCi/mmol) and cells incubated for 2 hours, washed with PBS and homogenized in Buffer A. The S15 was used for immunoprecipitation. About 10^7 cpm of S15 proteins were added to the pelleted
- 5 Portein A-Sepharose and mixed for 2 hours at 4°C. The Beads were washed with 1% BSA, 1% NP40, 2M KCl in PBS and twice with PBS only. Samples were analysed by sodium-dodecyl-sulphate-polyacrylamide gel electrophoresis.

10 EXAMPLE 18

USES OF ANTI-PEPTIDE ANTIBODIES TO DETECT THE (2'-5') OLIGO A SYNTHETASE ACTIVITY

- 15 Immunoprecipitation of the (2'-5') oligo A synthetase activity by anti-(2'-5') oligo A synthetase activity peptide antibodies

- The antiserum B was raised against a peptide common to the E16 and E18 sequences, while antiserum C was raised against a peptide found
- 20 only in E16. We used these antibodies to verify that they immunoprecipitate the (2'-5') oligo A synthetase activity specifically. The (2'-5') oligo A synthetase activity adsorbed on the immune IgG-Protein A Sepharose and that remaining in the supernatant were compared to the same fractions obtained by using non-immune IgG.
 - 25 Extracts from two cell lines which express preferentially either the 1.6 kb RNA (Wish cells) or the 1.8 kb RNA (Daudi cells) were compared. Antibodies C (E16-specific) were 20 times more efficient to adsorb the activity from Wish cells than normal serum. Subtracting the background with normal serum, allows to evaluate what is
 - 30 specifically bound to anti-B and anti-C (Fig. 16). Anti-C retained the (2'-5') oligo A synthetase activity from Wish cells but not from Daudi cells, in line with the absence of E16 mRNA and 40 kd protein in these cells (see Example 19). Anti-B adsorbed (2'-5') oligo A synthetase activity from both Daudi and Wish cell extracts.

- 35 The antibodies produced against peptides deduced from the cloned cDNAs, recognize, therefore, specifically different (2'-5') oligo A synthetase forms.

EXAMPLE 19IMMUNOBLOT ANALYSIS OF THE DIFFERENT FORMS OF (2'-5') OLIGO A
SYNTHETASE ACTIVITY FROM HUMAN CELLS

5 The antibodies against peptide B were tested for their ability to
bind specifically to (2'-5') oligo A synthetase activity in crude
extracts of human cells separated by sodium-dodecyl-sulphate-
polyacrylamide gel electrophoresis and blotted electrophoretically
10 onto nitrocellulose paper. In addition to being recognized by the
antibodies in immunoblots, we expect genuine (2'-5') oligo A synthe-
tase proteins present in extracts of these human cells to be
induced by IFN treatment, and we therefore looked only at the induced
proteins revealed by the immunoblots (Fig. 17).

15 The cell lines Daudi, Wish and SV80 were compared because of their
differences in the pattern of expression of the (2'-5') oligo A
synthetase mRNAs (see Example 18). Antibodies B detect as
expected a 45-46 kd protein similar in size to the E18 product, in
20 Daudi cells and no 40 kd which would correspond to E16 whose mRNA is
not expressed by Daudi cells. In contrast, the 40 kd E16 protein is
present in Wish cells without 46 kd E18 in line with the absence of
1.8 kb RNA in these cells. Both proteins are detected by anti-B in
SV80 cells. These results demonstrate that human cells produce the
25 40 and 46 kd proteins and this only when they express the 1.6 and
1.8 kb RNAs respectively.

The immunoblots with anti-B also reveal that there are not only two
forms of (2'-5') oligo A synthetase in human cells but
30 probably four different forms. This can be deduced from the fact
that in addition to the 40 and 46 kd proteins, anti-B clearly detect-
ed two other proteins of 100 kd and 67 kd which are induced by IFN
(Fig. 17 and 18). The 100 kd was not detected in Daudi cells, show-
ing that the large proteins detected by anti-B are also expressed in
35 a cell-specific pattern. The fact that the anti-B was raised against
a peptide derived from the sequence of genuine (2'-5') oligo A syn-
thetase forms, and that the two larger proteins are induced
by IFN, makes it very likely that they belong to the (2'-5') oligo A.

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1 synthetase system. To ascertain that these are (2'-5')
oligo A synthetase forms, we have purified (2'-5') oligo A
synthetase from different cellular fractions of SV80 and
followed in parallel the protein detected by antibodies B.

5

Separation of the different active forms of (2'-5') oligo A synthe-
tase.

The separation of the different protein species detected by anti-
bodies B is shown in Fig. 18 and 19. Most of the 40 kd protein remains
10 in the 100,000g supernatant (S100) of NP40 cytoplasmic extracts from
SV80 cells. It is not adsorbed on DEAE-cellulose in low salt and
adsorbs to CM-cellulose from which it elutes at high salt concen-
tration. In contrast, the 100 kd protein is almost absent from S100
15 and is concentrated in the microsomal pellet (P100) from which it can
be solubilized by Na deoxycholate (DOC) or 0.5M KCl. This protein
was adsorbed on DEAE-cellulose at low salt and elutes at high salt.
The 67 kd and 45-46 kd remain partly in S100 but are relatively con-
centrated per mg protein in the microsomal pellet. They appear to
20 be less readily extractable from microsomes by DOC or KCl.

Sedimentation on glycerol gradients showed that the activity purified
from S100 after CM-cellulose, parallels the sedimentation of the 40
kd protein E16. The fraction purified from P100 and eluted from
25 DEAE-cellulose, containing the 100 and 46 kd proteins, separated into
two peaks on glycerol gradients, sedimenting as 80,000 and 45,000 Mr
proteins. The (2'-5') oligo A synthetase in the heavy peak
parallels the presence of the 100 kd protein.

30 Different enzymatic properties of the various (2'-5') oligo A synthe-
tase activity forms

The 40 kd protein from the glycerol gradient has an optimal pH of 6.8
for its activity, and is only 25% as active at pH 7.8. Moreover, no
35 activity of the 40 kd (2'-5') oligo A synthetase can be obs-
erved at concentrations of poly (rI)(rC) lower than 1µg/ml and the
maximal activity requires 50-100µg/ml (Fig.20). The same high ds
RNA requirement was found for the E16 cDNA product produced by recom-

1 binant DNA technology in E.coli.

The 100 kd protein after the glycerol gradient, has an optimal pH of 7.6 for its (2'-5') oligo A synthetase and is less active at
5 acidic pH. It is maximally active already at extremely low concentrations of poly (rI)(rC) or in its absence, and its activity is even inhibited by high ds RNA concentrations. This strongly suggests that the different (2'-5') oligo A synthetase forms, because of
their different cytoplasmic localizations and enzymatic properties,
10 are used by the cells under different conditions.

Many observations suggest that the IFN-induced (2'-5') oligo A synthetase is involved in two distinct, seemingly opposite, phases of cell growth (cell cycling and growth inhibition) in addition to its possible role in the antiviral effect (reviewed in
15 Revel, 1984). This may be relevant to the issue of multiple (2'-5') oligo A synthetase forms. In synchronized cell cultures we have observed that (2'-5') oligo A synthetase behaves as a cell-cycle protein (Mallucci et al, 1985). Thus, synchronized cultures of Mouse embryo fibroblasts exhibit a sharp rise in (2'-5')
20 oligo A synthetase activity and (2'-5') oligo A synthetase mRNA at the end of the S-phase followed by a rapid disappearance of the RNA and enzyme activity when the cells proceed to G2. Anti-mouse IFN antibodies reduced the (2'-5') oligo A synthetase
25 induction. In this system we also observed that the (2'-5') oligo A synthetase RNA which accumulates in S-phase is a large 4-5 kb transcript different from the 1.7 kb RNA species which accumulates in the same cells when treated with exogenous IFN. This suggests that the S-phase (2'-5') oligo A synthetase is a different
30 form of the enzyme than that in cells growth-arrested by exogenously added IFN. Because of its large mRNA, it is likely to be like the 100 kd, a low ds RNA requiring form. Anti-B antibodies detected also the (2'-5') oligo A synthetase multiple forms in mouse cells.

35

These considerations illustrate the advantage of being able to assay independently the 4 forms of (2'-5') oligo A synthetase, which may vary individually in various physiological conditions and

1 diseases.

EXAMPLE 20

5 USE OF ANTI-(2'-5') OLIGO A SYNTHETASE ACTIVITY PEPTIDES ANTIBODIES
FOR IMMUNOASSAYS OF (2'-5') OLIGO A SYNTHETASE ACTIVITY

Since the anti-B antibodies recognizes all the forms of (2'-5') oligo
A synthetase, it can be used for an immunoassay of (2'-5')
10 oligo A synthetase in unfractionated extracts of human cells
either from cultures or directly obtained from patients.

An example of a solid-phase radio-immunoassay is shown in Fig. 21.
Wish and Daudi cells, either treated by IFN or untreated, were lysed
15 by the NP40-containing Buffer A and S15 prepared by microfuge cent-
rifugation as described above. Aliquots containing 1 to 10 μ g of
protein were directly applied to nitrocellulose paper (or to other
protein-binding paper) and the sheet treated with anti-B as for reg-
ular immunoblots (Example 19). The autoradiography in Fig. 11 shows
20 that ¹²⁵I-Protein A binds only to the samples originating from IFN-
treated cells. It is clear that this assay could be used also in
form of enzyme-linked immunoassay (ELISA) by replacing the labeled
Protein-A by Peroxydase or β -galactosidase conjugated anti-rabbit IgG.

25 The immunoassay of (2'-5') oligo A synthetase is rapid: 20
min for cell extract preparation, 2 hours for anti-B and Protein-A
adsorption and washing. The assay is sensitive and very small
amounts of cell extracts suffice to measure that (2'-5') oligo A syn-
thetase level. It is specific, no signal being obtained in
30 non-IFN treated cells.

EXAMPLE 21

35 IMMUNOFLUORESCENCE MICROSCOPY DETECTION OF (2'-5') OLIGO A SYNTHETASE IN CELLS

Enzymatic assays have established (see prior art) that (2'-5') oligo
A synthetase is elevated in peripheral blood mononuclear

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1 cells of patients with viral infections. The anti-(2'-5') oligo A
synthetase peptide antibodies can be used in immunofluor-
escence microscopy to detect (2'-5') oligo A synthetase
elevation in cells in general, and white blood cells in particular.

5 Blood (2 ml) was withdrawn from a healthy donor and from a patient
with acute viral illness. The mononuclear blood cells were separated
by Ficoll-Hypaque (Pharmacia) centrifugation, and spread on glass
coverslips directly or by the use of a cytospin microfuge (micro-
10 hematocrite). The cells were washed in PBS, fixed for 30 min in 3%
paraformaldehyde at room temperature (RT), rinsed with PBS and
treated with 0.5% Triton-X100 in Hank's salts for 5 min, rinsed again
with PBS and with PBS-2% gelatin. The coverslips were then incubated
with antiB serum diluted 1:5 in PBS-gelatin applied as a 40µl droplet
15 on parafilm onto which the coverslip were deposited. After 60 min
RT, the coverslips were rinsed in PBS-gelatin and FITC conjugated
anti-rabbit IgG (BioYeda) diluted 1:20 was applied by the parafilm
procedure. After 20 min at RT, coverslips were washed twice with
PBS-gelatin, then with H₂O and mounted on microscopic slides with
20 Miviol 4-88 (Hoechst)-Glycerol (2.5g Miviol, 6g Glycerol and 6 ml
H₂O to which 12 ml of 0.2M Tris.HCl pH 8.5 were added, followed by
incubation at 50°C and clarification 15 min at 5,000g). Parallel
coverslips were processed using normal rabbit serum instead of anti-
B. Slides were observed in a Zeiss fluorescence microscope and
25 photographed on Polaroid film with 30 seconds exposures.

Fig. 22 shows that the lymphocytes were stained with anti-(2'-5')
oligo A synthetase in blood samples from the patient with
viral infection but not in the blood of the healthy donor, where only
30 a low fluorescence of macrophages and granulocytes is seen. Normal
serum did not stain lymphocytes but also gave a low background in
macrophages/granulocytes. Thus, the present anti-(2'-5') oligo A
synthetase peptide antibodies can be used for microscopic
observation of cells, in cultures, blood and tissue sections, to
35 evaluate if the cells have reacted with interferon and have accumu-
lated (2'-5') oligo A synthetase.

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A. GRÜNECKER, Dipl.-Ing.

DR. H. KINKELDEY, Dipl.-Ing.

DR. W. STOCKMAIR, Dipl.-Ing. & E. KALTEFLUT

DR. K. SCHUMANN, Dipl.-Ing.

P. H. JAKOB, Dipl.-Ing.

DR. G. BEZOLD, Dipl.-Chem.

W. MEISTER, Dipl.-Ing.

H. HILGERS, Dipl.-Ing.

DR. H. MEYER-PLATH, Dipl.-Ing.

DR. M. BOTT-BODENHAUSEN, Dipl.-Ing.

DR. U. KINKELDEY, Dipl.-Ing.

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15 CLAIMS

1. A human DNA sequence coding for an enzyme having (2'-5')
oligo A synthetase activity.

20 2. A human DNA sequence according to claim 1, coding for an enzyme
having the amino acid sequence set forth in Fig. 7A.

3. A human DNA sequence according to claim 1, coding for an enzyme
having the amino acid sequence set forth in Fig. 7B.

25

4. A human DNA sequence according to claim 1, the enzyme con-
sisting of a C-terminal heptadecapeptide common to the amino acid
sequences mentioned in claims 2 and 3.

30 5. A human DNA sequence according to claim 1, showing the re-
striction map set forth in Fig. 9.

6. A sequence of (2'-5') oligo A synthetase cDNA set forth in
Fig. 7A being complementary to an 1.6 kb mRNA.

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7. A sequence of (2'-5') oligo A synthetase cDNA set forth in
Fig. 7B being complementary to an 1.8 kb mRNA.

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- 1 8. A DNA sequence which comprises the promoter of the DNA se-
quence according to one of the claims 1 to 5.
9. A DNA sequence according to claim 8, having the restriction
5 map set forth in Fig. 10.
10. A DNA sequence according to claims 8 or 9 having the DNA
sequence set forth in Fig. 11.
- 10 11. A 1.6 kb RNA having a nucleotide sequence complementary to
the nucleotide sequence set forth in Figure 7A.
12. A 1.8 kb RNA comprising a nucleotide sequence complementary
to the sequence of nucleotides 1-1322 set forth in Figure 7A and the
15 sequence of nucleotides 901-1590 set forth in Figure 7B.
13. A DNA transfer vector comprising an inserted DNA sequence
consisting essentially of the cDNA sequence of claim 6.
- 20 14. A DNA transfer vector according to claim 13, which is λ gt
11-E16 in which the inserted cDNA sequence has been fused in phase
with the lac Z gene suitable for expression of the coding sequence.
15. A DNA transfer vector comprising an inserted DNA sequence con-
25 sisting essentially of the cDNA sequence of claim 7.
16. A microrganism transformed by an expression vector according
to one of the claims 13 to 15.
- 30 17. A microorganism according to claim 16, which is Escherichia
coli.

- 1 18. An enzyme having (2'-5') oligo A synthetase activity and the amino acid sequence set forth in Figure 7A.
19. An enzyme having (2'-5') oligo A synthetase activity which
5 comprises the sequence of amino acids 1-364 set forth in Figure 7A and the sequence of amino acids 290-400 set forth in Figure 7B.
20. The enzyme of claim 18 comprising about 364 amino acids and having a molecular weight of about 41,500 daltons.
- 10 21. The enzyme of claim 19 comprising about 400 amino acids and having a molecular weight of about 46,000 daltons.
22. A method of monitoring the response of a patient to an inter-
15 feron, which comprises measuring the concentration of (2'-5') oligo A synthetase mRNA in cells or body fluids of the patient by hybridizing to the mRNA DNA complementary thereto.
23. The method of claim 22, wherein the mRNA is the 1.6 kb RNA
20 of claim 11.
24. The method of claim 22, wherein the mRNA is the 1.8 kb RNA of claim 12.
- 25 25. A method for evaluating the response of cells and tissues to interferon which comprises hybridizing RNA from cells or tissues exposed to interferon with cDNA complementary to the RNA, and determining the extent of hybridization.
- 30 26. A method according to claim 25, wherein the RNA is extracted from cells or tissues which have been exposed to interferon, immobilized on a membrane filter and hybridized to labelled cDNA specific for interferon-induced mRNAs.
- 35 27. A method according to claim 25, which comprises in situ hybridization of labelled cDNA to slices of tissues and evaluating by microscopic examination autoradiography, or fluorescence.

1 28. A method according to claim 25, wherein the cells or tissues are of human origin.

29. A kit for carrying out a method according to claim 25, containing a cDNA complementary to a sequence set forth in Figure 7A or 7B, reagents to carry out the hybridization tests for nick-translation with deoxyribonuclease I and [³²P]-gamma-dCTP, reagents for hybridization on nitrocellulose membranes, and reagents for RNA extraction from cells.

10

30. An antigenic peptide having an amino acid sequence contained within the amino acid sequence set forth in Figure 7A.

31. An antigenic peptide having an amino acid sequence contained within the sequence of amino acids 1-364 set forth in Figure 7A and the sequence of amino acids 290-400 set forth in Figure 7B.

32. The antigenic peptide of claim 30, having the amino acid sequence comprising the 17 C-terminal amino acids of the amino acid sequence set forth in Figure 7A and having the amino acid sequence:
20 ARG-PRO-PRO-ALA-SER-SER-LEU-PRO-PHE-ILE-PRO-ALA-PRO-LEU-HIS-GLU-ALA.

33. An antigenic peptide of claim 30, having the amino acid sequence:
25 GLU-LYS-TYR-LEU-ARG-ARG-GLN-LEU-THR-LYS-PRO-ARG-PRO-VAL-ILE-LEU-ASP-PRO-ALA-ASP.

34. An antibody raised against the antigenic peptide of claim 30, which recognizes and immunoprecipitates (2'-5') oligo A synthetase.
30

35. An antibody raised against the antigenic peptide of claim 31 which recognizes and immunoprecipitates (2'-5') oligo A synthetase.

35 36. An antibody according to one of the claims 34 or 35 against all four of the 40 KD, 46 KD, 67 KD and 100 KD forms of (2'-5') oligo A synthetase.

- 1 37. An antibody of claim 36, said antibody being obtained by
immunizing an animal with peptide B.
38. An antibody of claim 36, said antibody being conjugated with
5 a label to form a labeled antibody.
39. An antibody of claim 38, wherein the label is a fluorescent
label.
- 10 40. An antibody of claim 38, wherein the label is a radioactive
label.
41. An antibody of claim 38, wherein the label is an enzyme.
- 15 42. An assay for the 40 KD, 46 KD, 67 KD and 100 KD forms of
(2'-5') oligo A synthetase in cells which comprise incubat-
ing the cells with the labeled antibody of claim 38 and detecting
cells bearing (2'-5') oligo A synthetase activity in any of said
forms by means of said label.
- 20 43. An assay of claim 42 in which the assay is a fluorescent
immunoassay.
44. An assay of claim 42 in which the assay is a radioimmunoassay
- 25 45. An assay of claim 42 in which the assay is an enzyme immuno-
assay.
46. An assay of claim 42 in which the cells are mononuclear
30 blood cells.
47. A kit for the detection of all four forms of (2'-5') oligo A
synthetase in cells comprising the antibody of claim 38.
- 35 48. A 67 KD (2'-5') oligo A synthetase protein in a
state of enhanced purity.

1 49. A 100 KD (2'-5') oligo A synthetase protein in a
state of enhanced purity.

50. An antibody against one of the 40 KD, 46 KD, 67 KD or 100 KD
5 forms of (2'-5') oligo A synthetase which does not cross-
react with the other three forms.

51. A method of monitoring interferon activity in a subject
which comprises measuring the amount of (2'-5') oligo A synthetase
10 in a cell or body fluid of the subject at predetermined time
intervals, determining the differences in the amount of said synthe-
tase in the cell or body fluid of the subject within the different
time intervals, and determining therefrom the amount of synthetase
in the cell or body fluid of the subject and thereby the interferon
15 activity of the subject.

52. The method of claim 51, wherein the amount of synthetase is
measured by contacting the synthetase with the antibody of claim 34
so as to form a complex therewith and determining the amount of
20 complex so formed.

53. The method of claim 52 further comprising the extraction of
(2'-5') oligo A synthetase from a cell or body fluid which has been
exposed to interfereon, labelling the extracted synthetase with an
25 identifiable marker to form a labelled synthetase, contacting the
labelled synthetase with the antibody under suitable conditions so
as to form a labelled-synthetase-antibody complex, and detecting
the marker in the complex, thereby detecting the synthetase.

30 54. The method of claim 53 wherein the marker is ³⁵S-methionine.

55. A kit for carrying out the method of claim 53, comprising
the antibody of claim 34 or 35, materials for extracting the synthe-
tase, materials for labelling the synthetase, and materials for de-
35 tecting the marker and determining the amount of synthetase.

56. Cloned DNA that specifically hybridizes to messenger RNAs
which appear in human cells after exposure to interferon.

1 57. Cloned cDNA according to claim 56 specific for the (2'-5')
oligo A synthetase mRNAs of 3.6, 1.8 and 1.6 kilobase.

58. Cloned DNA according to claim 56 specific for the mRNA of a
5 56,000 Mr-protein, which mRNA is 2 kilobase and which has the
nucleotide sequence set forth in Figure 1.

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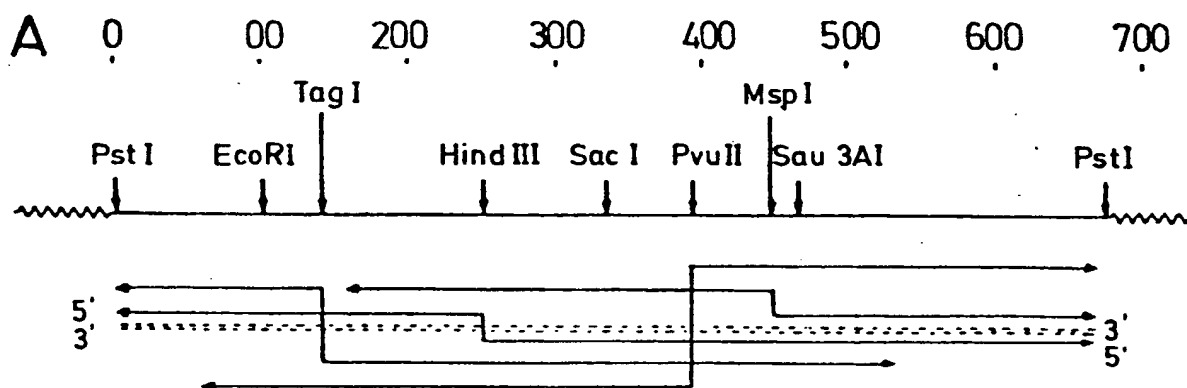


FIG. 1A

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B
 TTT CGG ACG GTC TTG GAA TTA GTC ATA AAC 30 TAC CAG CAA CTC TGC ATC TGC TAC TGG ACA AAG 50
 PHE ARG THR VAL LEU GLU LEU VAL ILE ASN 90 TYR GLN GLN LEU CYS ILE TYR TRP THR LYS 120
 TAT TAT GAC TTT AAA AAC CCC ATT ATT GAA 90 AAG TAC CTG AGA AGG CAG CTC ACG AAA CCC
 TYR TYR ASP PHE LYS ASN PRO ILE ILE GLU 150 LYS TYR LEU ARG ARG GLN LEU THR LYS PRO 180
 AGG CCT GTG ATC CTG GAC CCG GCG GAC CCT 210 ACA GGA AAC TTG GGT GGT GGA GAC CCA AAG
 ARG PRO VAL ILE LEU ASP PRO ALA ASP 210 THR GLY ASN LEU GLY GLY ASP PRO LYS 240
 GGT TGG AGG CAG CTG GCA CAA GAG GCT GAG 270 GCC TGG CTG AAT TAC CCA TGC TTT AAG AAT
 GLY TRP ARG GLN LEU ALA GLN GLU ALA 300 GGC TGG CTG AAT TAC CCA TGC TTT AAG AAT
 TGG GAT GGG TCC CCA GTG AGC TCC TGG ATT 330 CTG CTG GTG AGA CCT CCT GCT TCC TCC CTG
 TRP ASP GLY SER PRO VAL SER SER TRP ILE LEU LEU VAL ARG PRO PRO ALA SER SER LEU 360
 CCA TTC ATC CCT GCC CCT CTC CAT GAA GCT TGA GAC ATA TAG CTG GAG ACC ATT CTT TCC
 PRO PHE ILE PRO ALA PRO LEU HIS GLU ALA 390
 AAA GAA CTT ACC TCT TGC CAA AGG CCA TTT ATA TTC ATA TAG TGA CAG GCT GTG CTC CAT 420
 ATT TTA CAG TCA TTT TGG TCA CAA TCG ACG GTT TCT GGA ATT TTC ACA TCC CTT GTC CAG 430
 AAT TCA TTC CCC TAA GAG TAA TAA ATA ATC TCT AAC ACC AAA 510

FIG.1B

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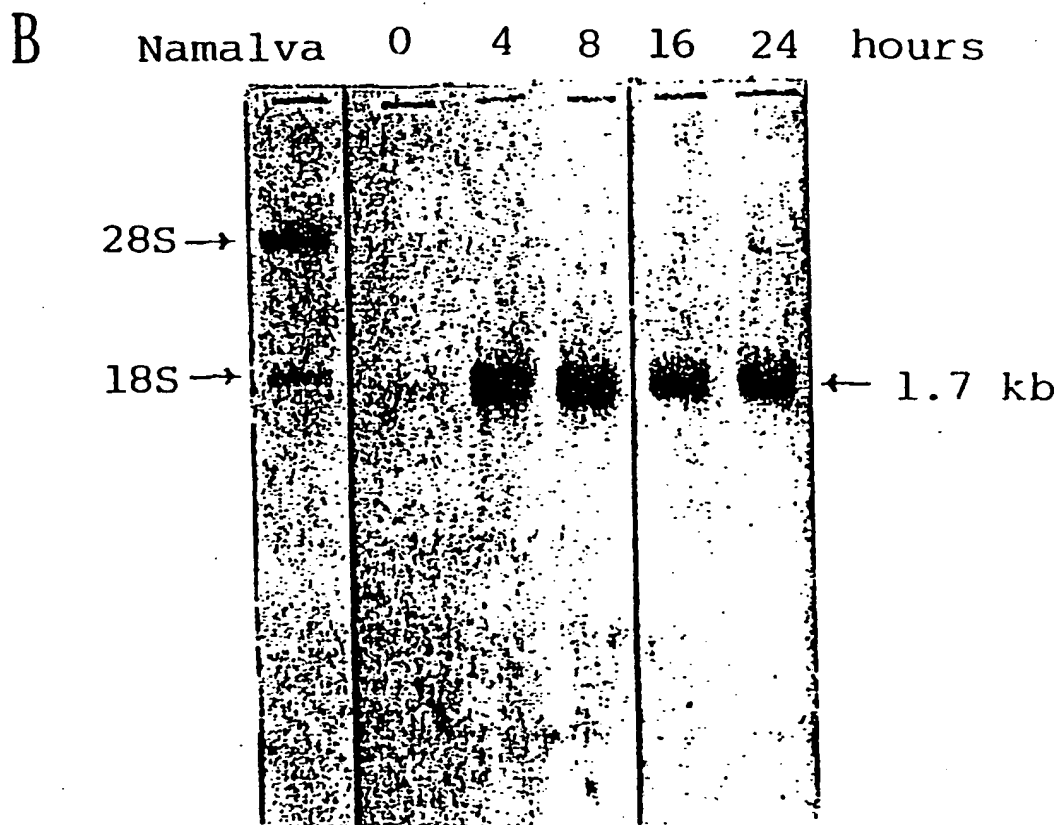
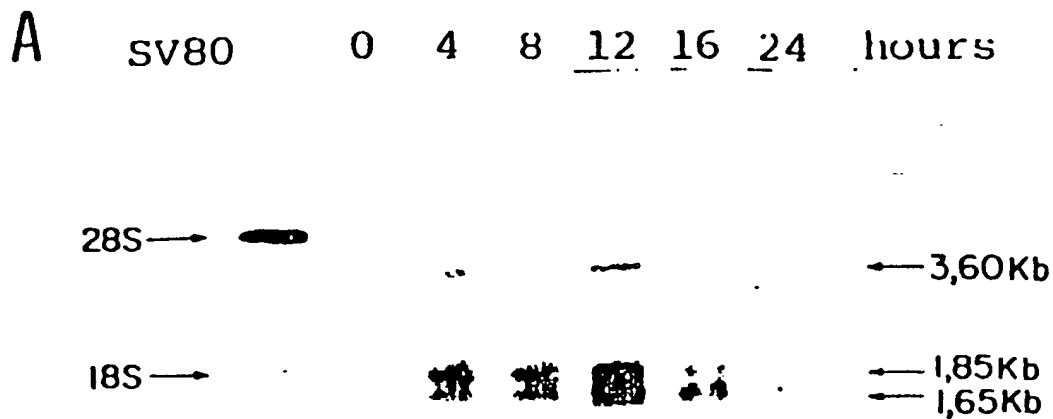


FIG.2

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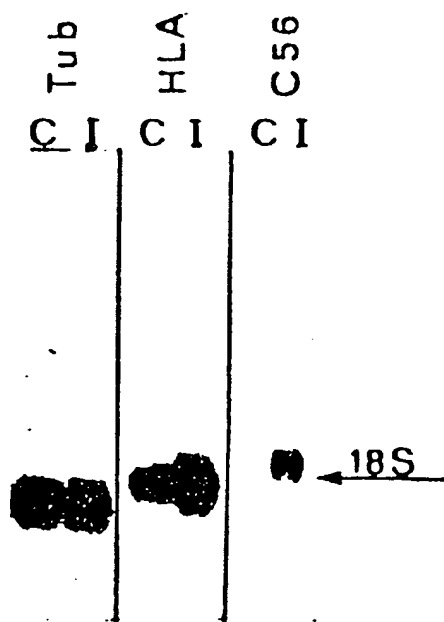


FIG.3

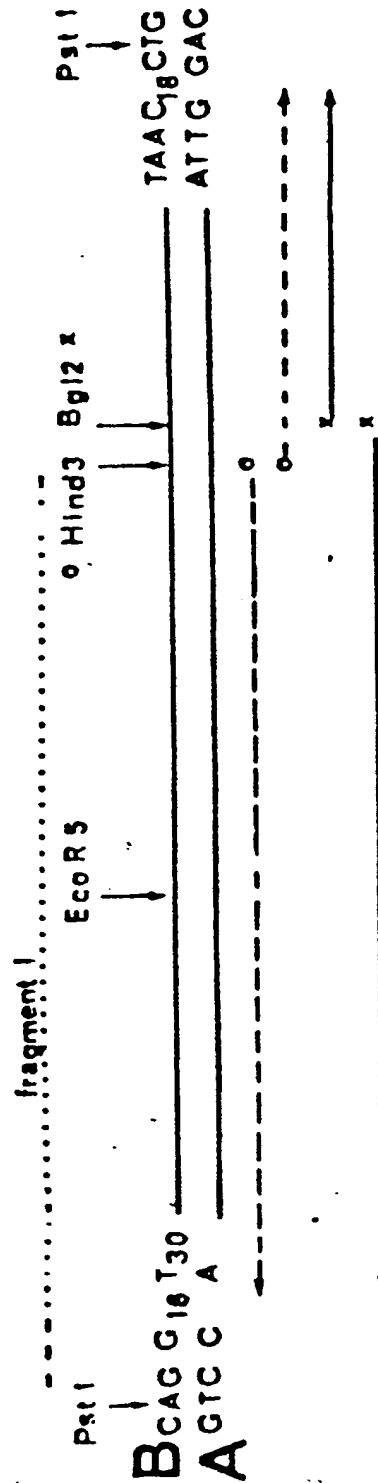


FIG. 4A

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B

30 60
TIA ACA AGG GAT AAA AGT ATC AAT TCT TTG AAG AAA TTG GTT TTA AGG AAA CTT CGG AGA
THR ARG ASP LYS SER ILE ASN SER LEU LYS LYS LEU VAL LEU ARG LYS LEU ARG ARG

90 120
AAG GCA TTA GAT CIG GAA AGC TTG AGC CTC CTT GGG TTC GTC TAC AAA TTG GAA GGA AAT
LYS ALA LEU ASP LEU GLU SER LEU SER LEU GLY PHE VAL TYR LYS LEU GLU GLY ASN

130 180
ATG AAT GAA GCC CIG GAG TAC TAT GAG CGG GCC CTG AOA CTG GCT GCT GAC TTT GAG AAC
MET ASN GLU ALA LEU GLU TYR TYR GLU ARG ALA LEU ARG LEU ALA ASP PHE GLU ASN

210 240
TCT GTG AGA CAA GGT CCT TAG GCA CCC AGA TAT CAG CCA CTT TCA CAT TTC ATT TCA TTT
SER VAL ARG GLN GLY PRO END

270 300
TAT GCT AAC ATT TAC TAA TCA TCT TTT CIG CTT ACT GTT TTC AOA AAC ATT ATA ATT CAC

330
TGT AAT GAT GTA ATT CTT GAA TAA TAA ATC TGA CAA AAT ATT (A)_n

FIG. 4B

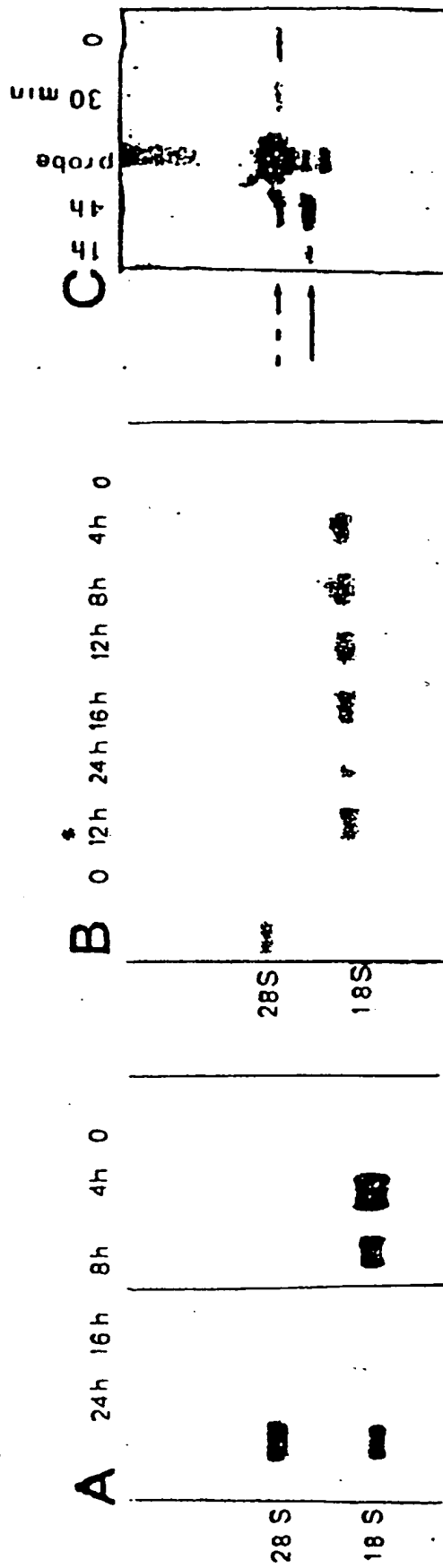


FIG. 5

A. 1.6 kb EcDNA

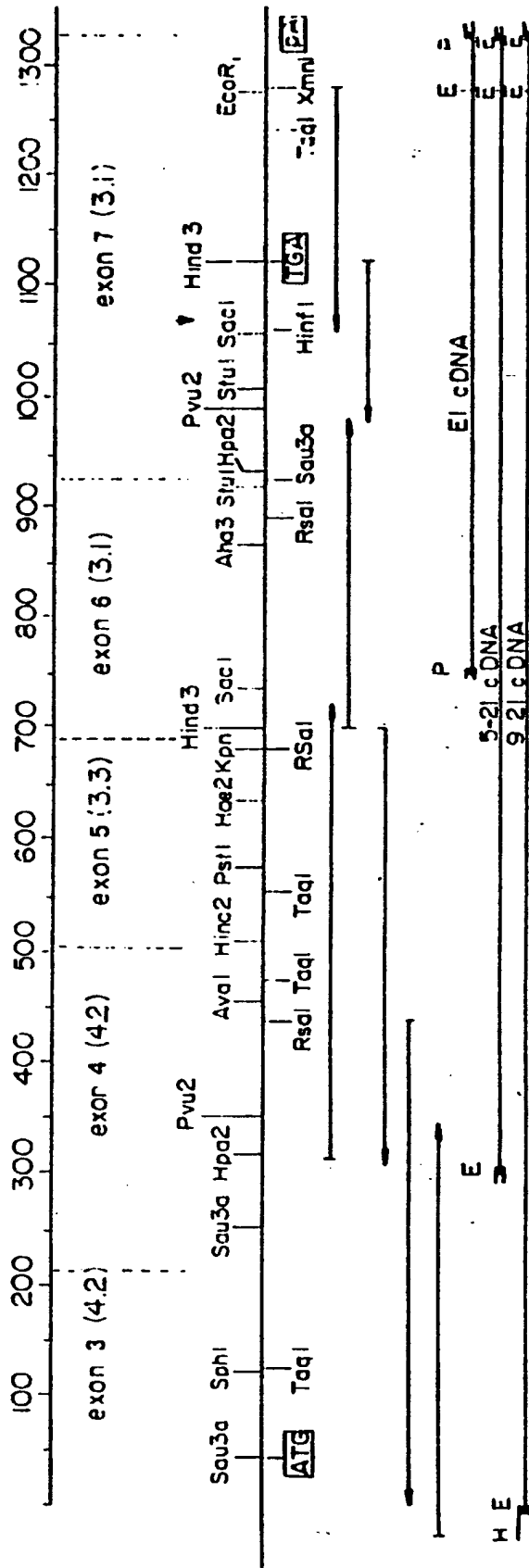


FIG. 6A

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B. 1.8kb EcDNA

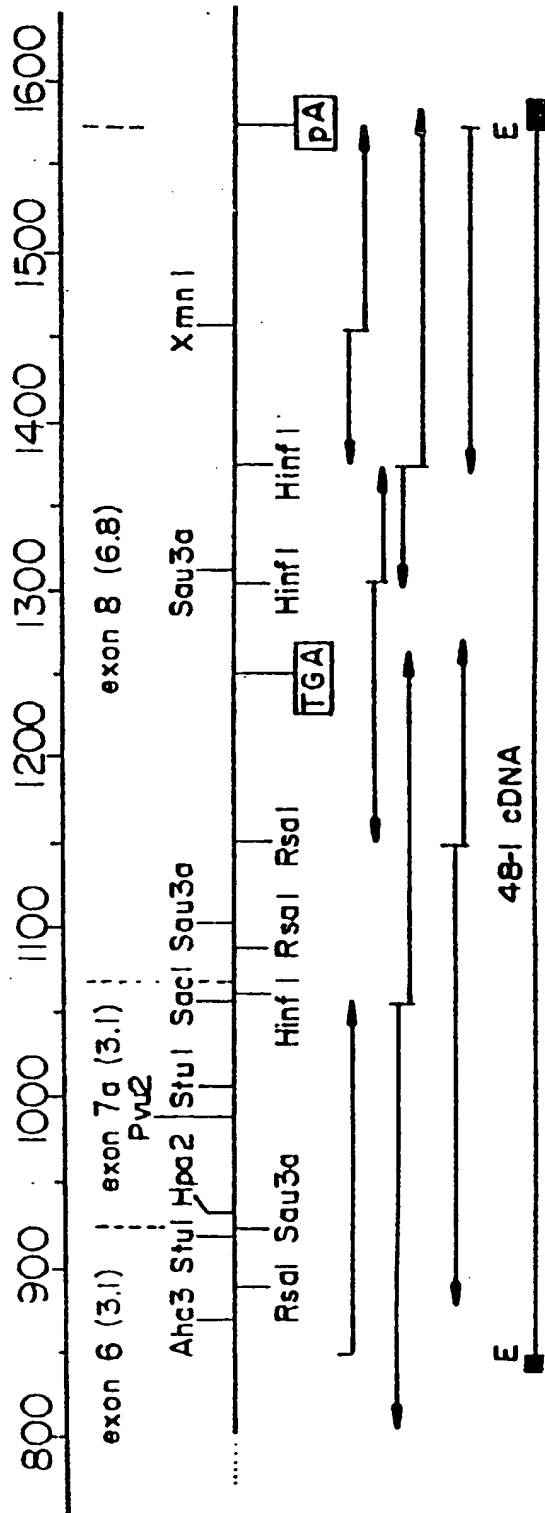


FIG. 6B

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1 E16..GAG GCA GTT CTG TTG CCA CTC TC1 CTC CTG TCA ATG ATG CAT CTC AGA AAT ACC CCA GCC AAA TC1 CTG GAC AAG TTC ATT GAA GAC TAT 90
 91 120 Sph1 30 (1) Sau3a
 E16 CTC TTG CCA GAC ACG TGT TTC CGC ATG CAA ATC GAC CAT GCC ATT GAC ATC ATC TGT TGT TGC TGC CCA COT ACC 180
 LEU LEU PRO ASP THR CYS PHE ARG MET GLN ILE ASP HIS ALA ILE ASP ILE ILE CYS GLY PHE LEU LYS GLU ARG CYS PHE ARG GLY SER 270
 181 210 (61) 24C
 E16 TCC TAC CCT CTG TGT TGT TCC AAG GTG GTA AAGTGGT GGC TCC TCA GGC AAG GGC ACC ACC CTC AGA GGC CCA TCT GAC GCT GAC CTG GTT 270
 SER TYR PRC VAL CYS VAL SER LYS VAL LYS GLY SER SER GLY LYS GLY THR THR LEU ARG GLY ARG SER ASP ALA ASP LEU VAL 360
 271 300 (91) 33C
 E16 GTC TTC CTC AGT CCT CTC ACC ACT TTT CAG CAT CAG TTA AAT CCC CGG GGA GAG TTC ATC CAG GAA ATT ACG AGA CAG CTG GAA GCC TGT 360
 VAL PHE LEU SER PRO LEU THR THR PHE GLN ASP GLN LEU ASN ARG ARG GLY GLU PHE ILE GLN GLU ILE ARG ARG GLN LEU GLU ALA CYS 450
 361 390 (121) 42C
 E16 CAA ACA GAG AGA CCA CTT TCC GTG AAG TTT GAG GTC CAG CCT CCA CGC TCG GGC AAC CCC CGT CGG CTC AGC TTC GTA CTG AOT TCG CTC 450
 GLN ARG GLU ARG ALA LEU SER VAL LYS PHE GLU VAL GLN ALA PRC ARG TRP GLY ASN PRC ARG ALA LEU SER PHE VAL LEU SER SER LEU 540
 451 480 (151) 51C
 E16 CAG CTC GGG GAG GGG GTG GAG TTC GAT GTG CTC CTT GGC TTT GAT GGC CTG GGT CAG TTG ACT GGC AGC TAT AAA CCT AAC CCC CAA ATC 540
 GLN LEU GLY GLU GLY VAL GLU PHE ASP VAL LEU PRO ALA PHE ASP ALA LEU GLY GLN LEU THR GLY SER TYR LYS PRC ASN PRC GLN ILE 630
 541 570 Pst1(181) 60C
 E16 TAT GTC AAG CTC ATC GAG GAG TGC ACC GAC CTG CAG AAA GAG GGC GAG TTC TCC ACC TCC TTC ACA GAA CTA CAG AGA GAC TTC CTG AAG 630
 TYR VAL LYS LEU ILE GLU GLU CYS THR ASP LEU LEU GLN LYS GLU GLY GLU PHE SER THR CYS PHE THR GLU LEU GLN ARG ASP PHE LEU LYS 720
 631 660 (211) 69C
 E16 CAG CGC CCC ACC AAG CTC AAG AGC CTC ATC CGC CTA GTC AAG CAC TCG TAC CAA AAT TGT AAG AAG AAG CTT CGG AAG CTG CCA CCT CAG 720
 GLN ARG PRC THR LYS LEU LYS SER LEU ILE ARG LEU VAL LYS HIS TRP TYR GLN ASN CYS LYS LYS LEU GLY LYS LEU PRC PRO GLN 810
 721 750 (241) 78C
 E16 TAT GGC CTG GAG CTC CTG ACG GTC TAT CTT TCG GAG CCA GGG AGC ATG AAA ACA CAT TTC AAC ACA GCC CAA CCA TTT CGG ACG GTC TTG 810
 TYR ALA LEU GLU LEU LEU THR VAL TYR ALA TRP GLU ARG GLY SER MET LYS THR HIS PHE ASN THR ALA GLN GLY PHE ARG THR VAL LEU 900
 811 840 (271) 87C
 E16 GAA TTA GTC ATA AAC TAC CAG CAA CTC TGC ATC TAC TCG ACA AAG TAT TAT GAC TTT AAA AAC CCC ATT ATT GAA AAG TAC CTG AGA ACG 900
 GLU LEU VAL ILE ASN TYR GLN GLN LEU CYS ILE TYR TRP THR LYS TYR TYR ASP PHE LYS ASN PRO ILE ILE GLU LYS TYR LEU ARG ARG 990
 901 930 (301) 96C
 E16 CAG CTC ACG AAA CCC ACG CCT GTG ATC CTG GAC CCG GCG GAC CCT ACA CCA AAG TTG GGT GGT CGA GAC CCA AAG GGT TCG ACG CAG CTG 990
 GLN LEU THR LYS PRO ARG PRC VAL ILE LEU ASP PRC ALA ASP PRC THR GLY ASN LEU GLY GLY ASP PRC LYS GLY TRP ARG GLN LEU 1080
 991 1020 (331) 105C
 E16 GCA CAA GAG GCT GAG GGC TCG CTG AAT TAC CCA TCC TTT AAG AAT TCG GAT GGC TCC CCA GTG ACG TCC TCG ATT CTG CTG GTG AGA CCT 1080
 ALA GLN GLU ALA GLU ALA TRP LEU ASN TYR PRC CYS PHE LYS ASN TRP ASP GLY SER PRC VAL SER TRP ILE LEU LEU VAL ARG PRC 1170
 1081 1110 (361) 114C
 E16 CCT GCT TCC TCC CTC CCA TTC ATC CCT GCT CCT CAT GAA GCT TGA GAC ATA TAG CTG CAG ACC ATT CTT TCC AAA GAA CTT ACC TCT 1170
 PRO ALA SER SER LEU PRC PHE ILE PRC ALA PRC LEU HIS GLU ALA END 1260
 1171 1200 123C
 E16 TCC CAA ACG CCA TTT ATA TTC ATA TAG TCA CAG GCT GTG CTC CAT ATT TTA CAG TCA TTT TCG TCA CAA TCG ACG GTT TCT CCA ATT TTC 1260
 1261 1290 132C
 E16 ACA TCC CTT GTC CAG AAT TCA TTC CCC TAA GAG TAA TAA ATA ATC TCT AAC ACCAAAAA... 1350

7B

SEQUENCE OF cDNA FOR E 1.8 Kb RNA (E18, clone 48-1)

9C1 exon 6 lexon 7a Sau3a 930 (301) 960 Pvu2 990
 E18 CAG CTC ACG AAA CCC ACG CCT GTG ATC CTG GAC CCG GCG GAC CCT ACA GGA AAC TTG GGT GGT GGA GAC CCA AAG GGT TCG AGG CAG CTG
 ..GLN LEU THR LYS PRC ARG PRC VAL ILE LEU ASP PRC ALA ASP PRC THR GLY ASN LEU LEU GLY GLY ASP PRO LYS GLY TRP ARG GLN LEU

 991 1020 (331) 1050 Sac1 exon 7a lexon 8 1080
 E18 GCA CAA CAG GCT GAG GCC TGG CTG AAT TAC CCA TCG TTT AAG AAT TCG GAT GGG TCC CCA GTG ACG TCC TCG ATT CTG CTGCTT GAA ACC
 ALA GLN GLU ALA GLU ALA TRP LEU ASN TYR PRC CYS PHE LYS ASN TRP ASP GLY SER PRC VAL SER SER TRP ILE LEU LEU ALA GLU SER

 1051 (glyc.) 1110 (361) 1140
 E18 AAC AGT ACA GAC GAT GAG ACC GAC GAT CCC AGG ACC TAT CAG AAA TAT GGT TAC ATT GGA ACA CAT GAG TAC CCT CAT TTC TCT CAT AGA
 ASN SER THR ASP ASF GLU THR ASP PRC ARG THR TYF GLN LYS TYR GLY TYR ILE GLY THR HIS GLU TYR PRC HIS PHE SER HIS ARG
 1171 1200 (391) 1230
 E18 CCC AGC CTC CAG GCA GCA TCC ACC CCA CAG GCA GAA GAG GAC TGG ACC TCG ACC ATC CTC TGA ATG CCA GTG CAT CTT GGG GGA AAG
 PRC SER THR LEU GLN ALA ALA SER THR PRC GLN ALA GLU GLU ASP TRP THR CYS THR ILE LEU END
 1261 1290 Sau3a 1320
 E18 GGC TCC ACT GTT ATC TGG ACC AGT TCC TTC ATT TTC ACG TGG GAC TCT TGA TCC ACA GAA GAC AAA GGT CCT CAG TGA GCT GGT GTA TAA
 1351 1380 1410
 E18 TCC AAG ACA GAA CCC AAG TCT CCT GAC TCC TGG CCT TCT ATC CTA TCA TAG ATA ACA TTC TCC ACA GGC TCA CTT CAT TCC
 1441 Xmn1 1500
 E18 ACC TAT TCT CTG AAA ATA TTC CCT GAG ACA GAA CAG ACA GAT TTA GAT AAG ACA ATG AAA TTC CAG CCT TGA CTT TCT TCT GTG CAC CTG
 1531 1560
 E18 ATG GGA GCG TAA TGT CTA ATG TAT TAT CAA TAA CAA TAA TAA ACC AAA TAC CAAAA...

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FIG. 7B

HYDROPATHY PLOT OF THE C-TERMINI OF THE TWO (2'-5') OLIGO A SYNTHETASES

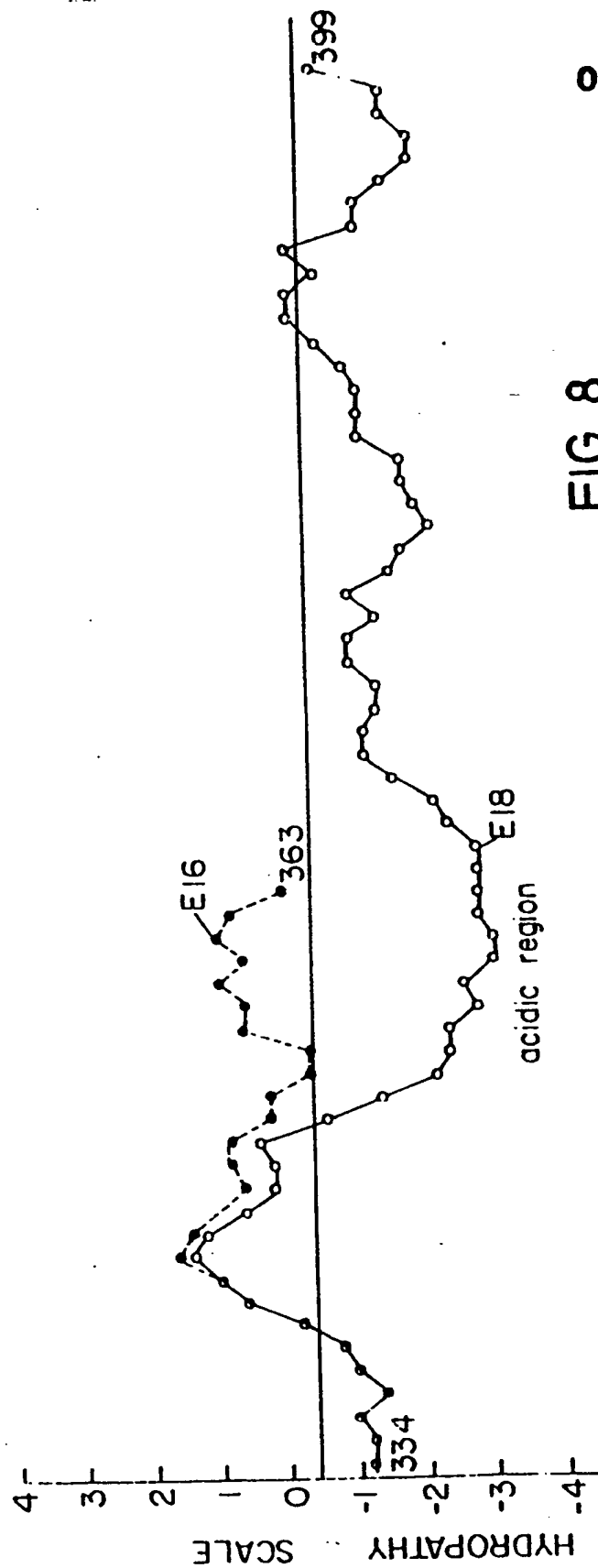


FIG. 8

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Human (2'-5') oligo A synthetase genomic clone Eλ28

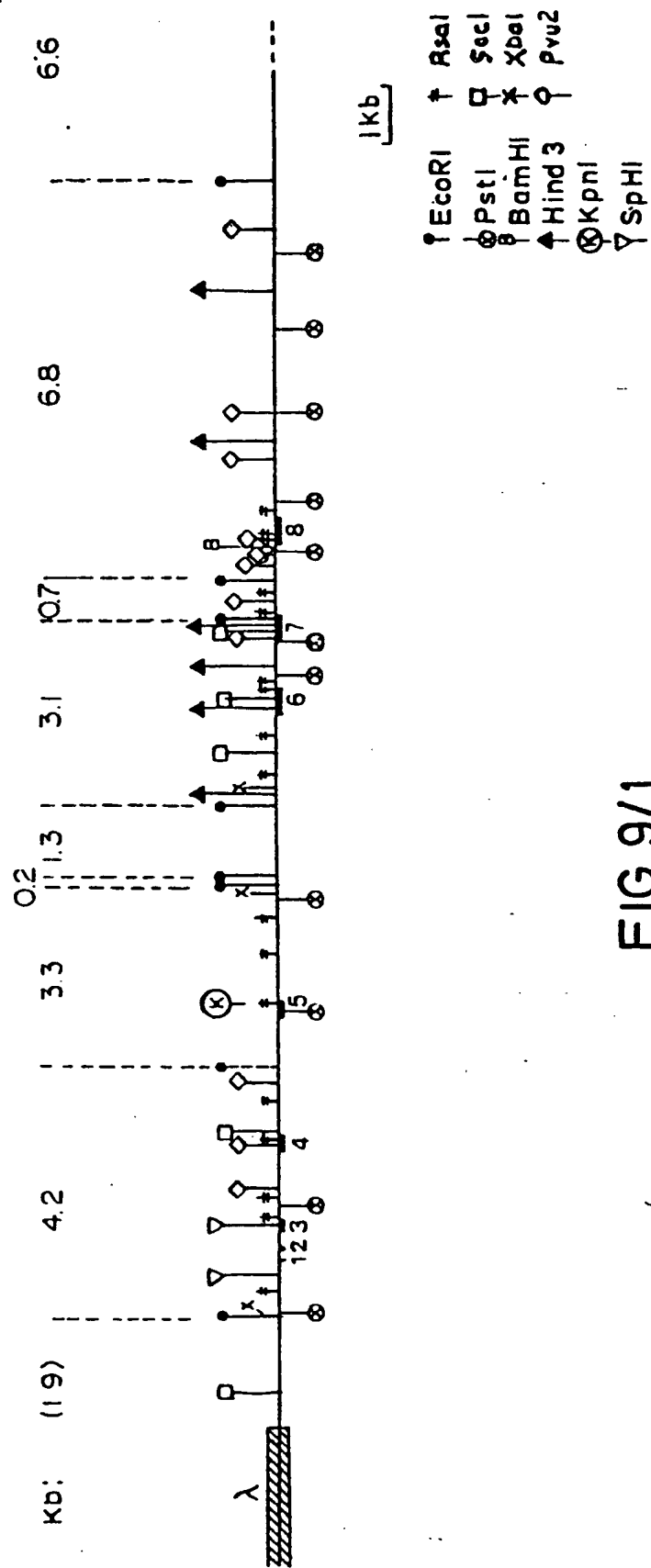


FIG.9/1

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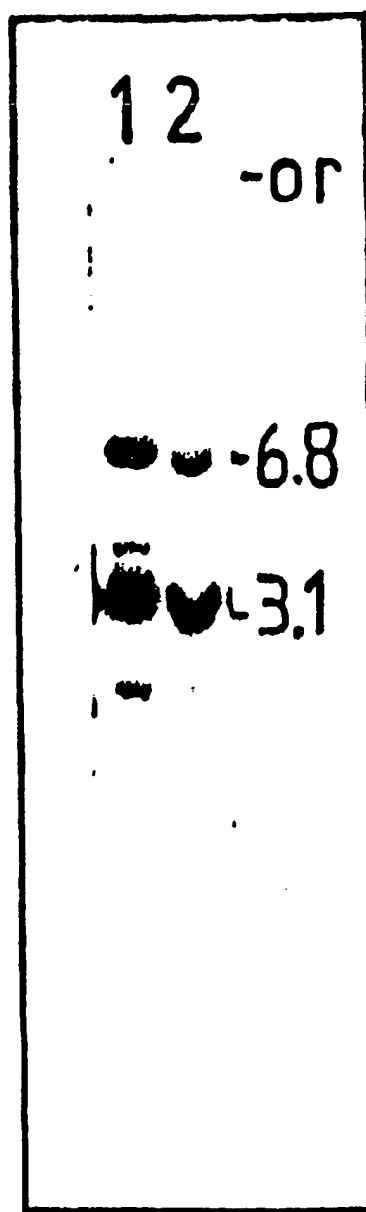


FIG.9/2

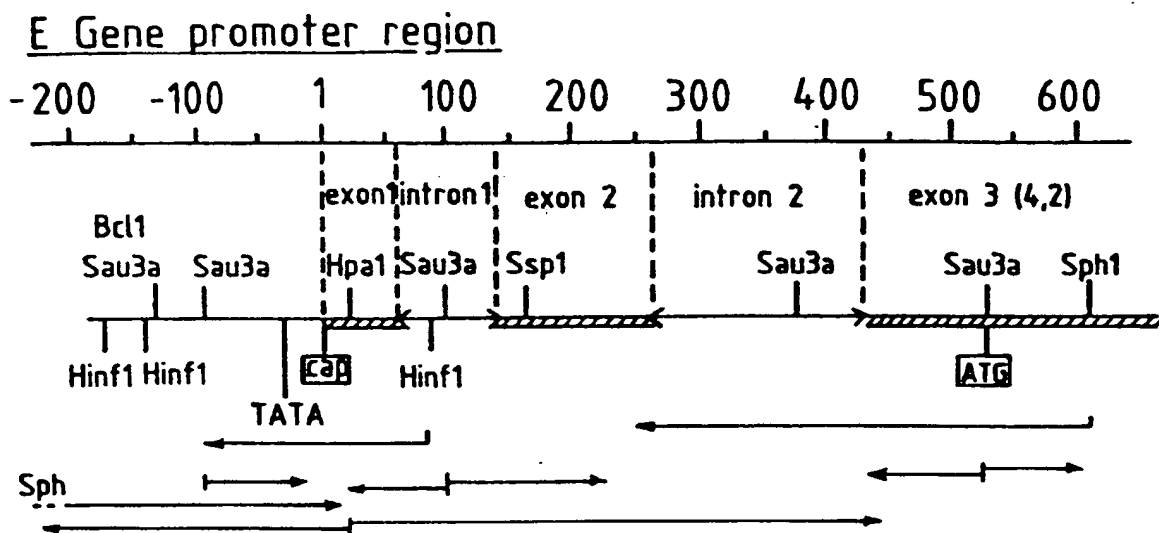


FIG.10

PROMOTER REGION OF THE HUMAN (2'-5') OLIGO A SYNTHETASE GENE

		-80	-70	-60	-50	-40	
E	Sau3a	CTCCAAAAA	TAATAAATA	AAATAAAAT	CTACTAATTG	AAACGGAAA	AAG-----
		-130			-90		-50
IFN- β		AAATAAAGAG	TTTAGAAG	TACTAAATG	AGGAAACTG	AAACGGAGAA	GTGAAAGTGG GAAATTCCTC TCAATAGAGA
		-30	-20	-10	1	10	30
E		AGTATAATA	CCATTCTTAA	CAAAAAGAAA	AGAGACCTGT	GTTCGTGTGT	GTGTTAACAT TTGAAAAAAA
		-40			-20		20
IFN- β		GAGGACCATC	TCATATAAT	AGGCCATACC	CATGGAGAAA	CGACATTCTA	ACTGCAACCT TTCGAAGCCT TTGCTCTGGC
		=====					

FIG. 11

Immunoprecipitation of (2'-5')oligoA Synthetase

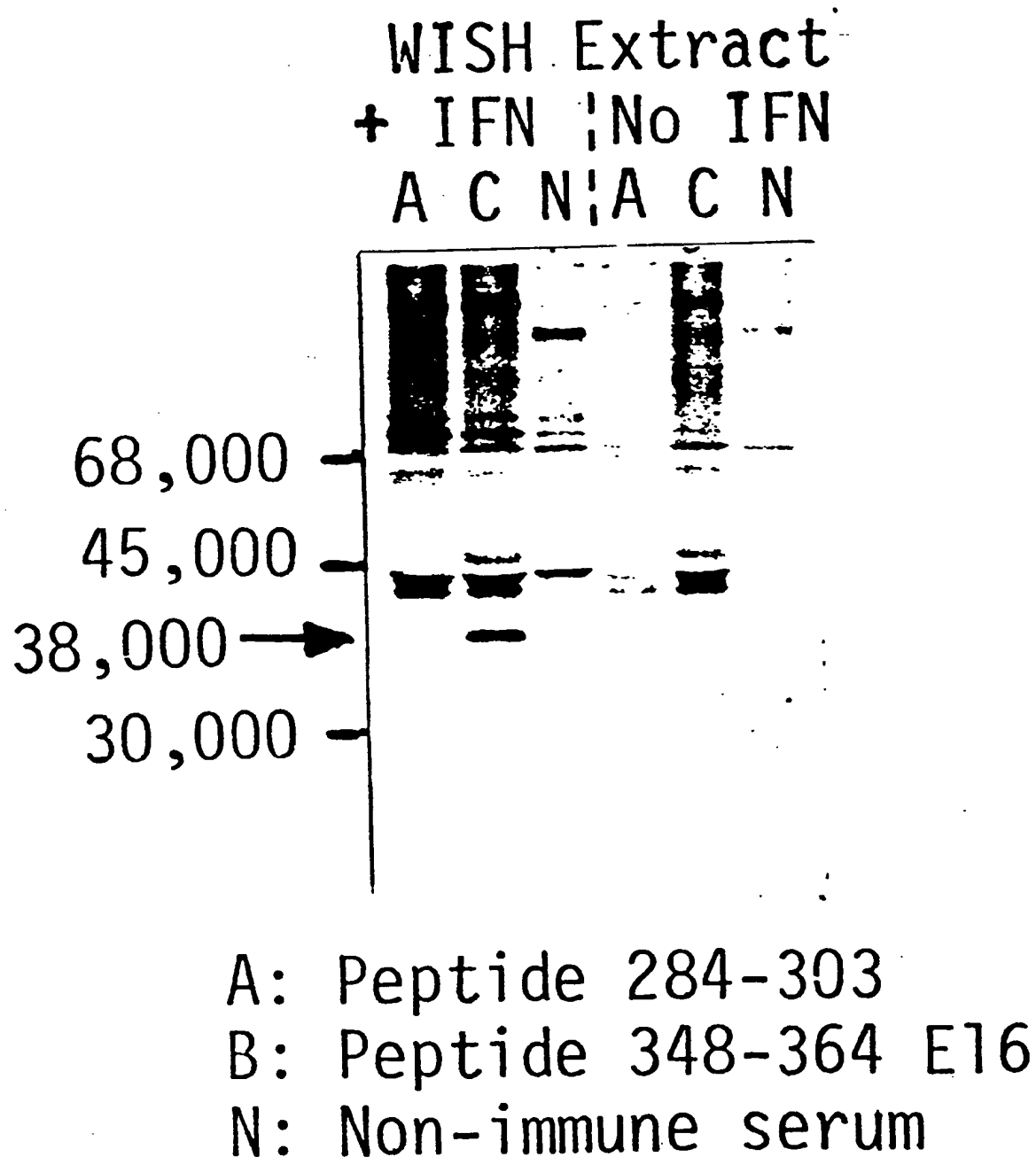


FIG. 12

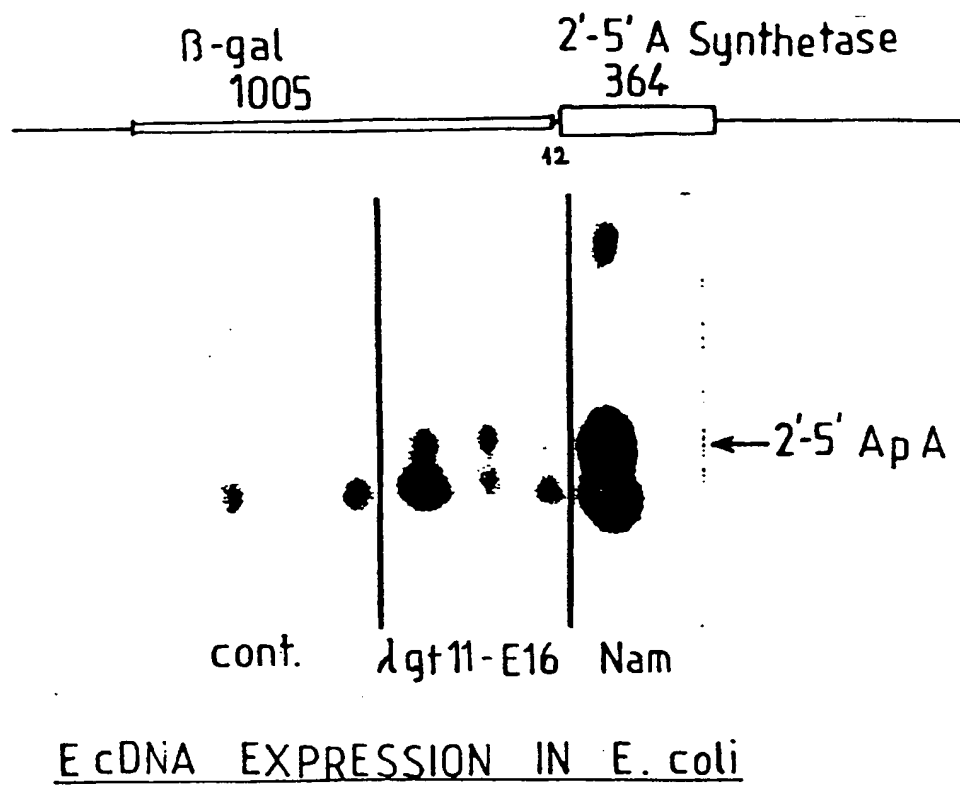


FIG.13

QUICK CELL BLOT FOR MEASURE OF (2'-5') OLIGO A SYNTHETASE RNA

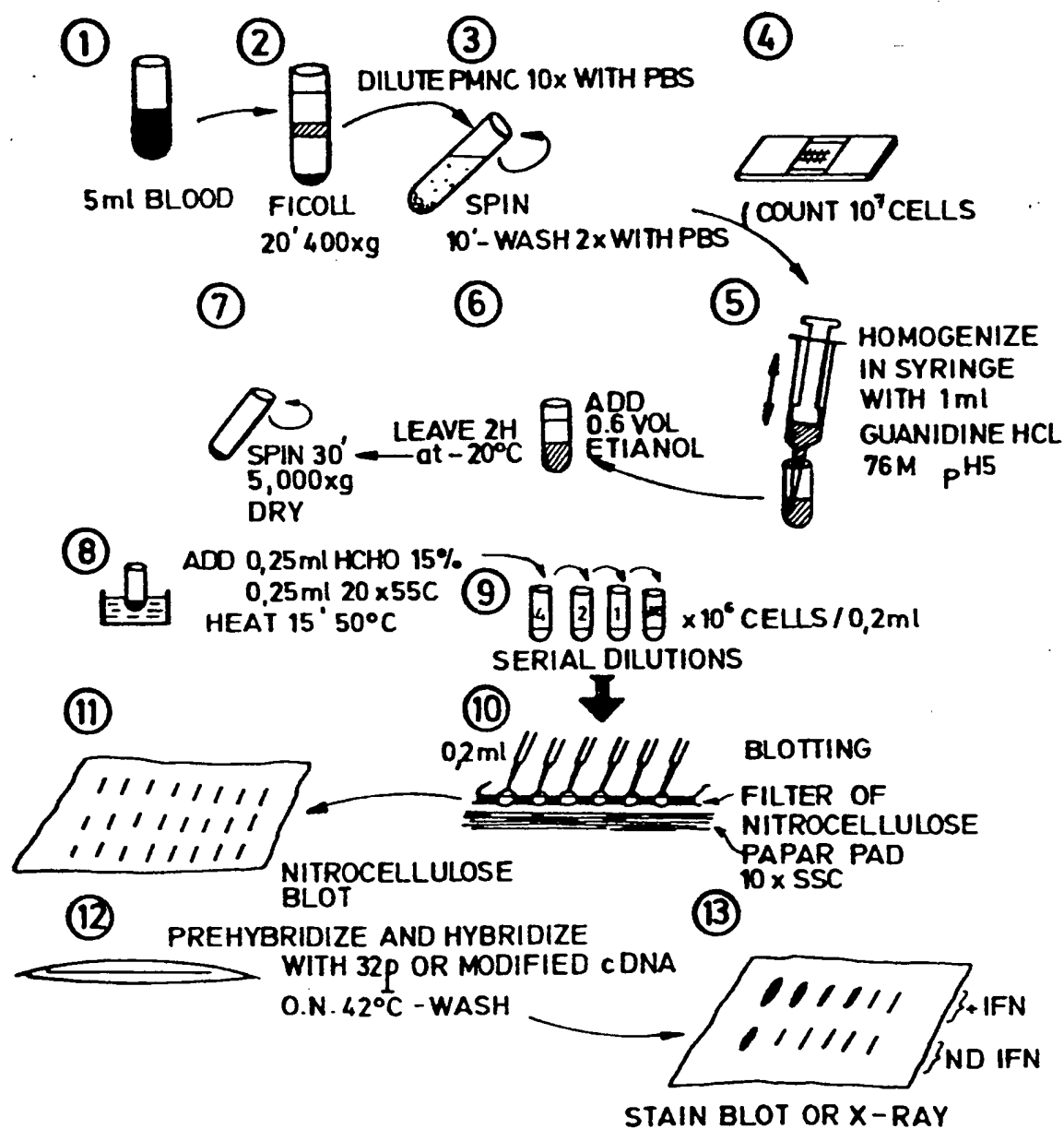


FIG.14

QUICK CELL BLOT FOR (2'-5') A
SYNTHETASE RNA

LYMPHOCYTES:

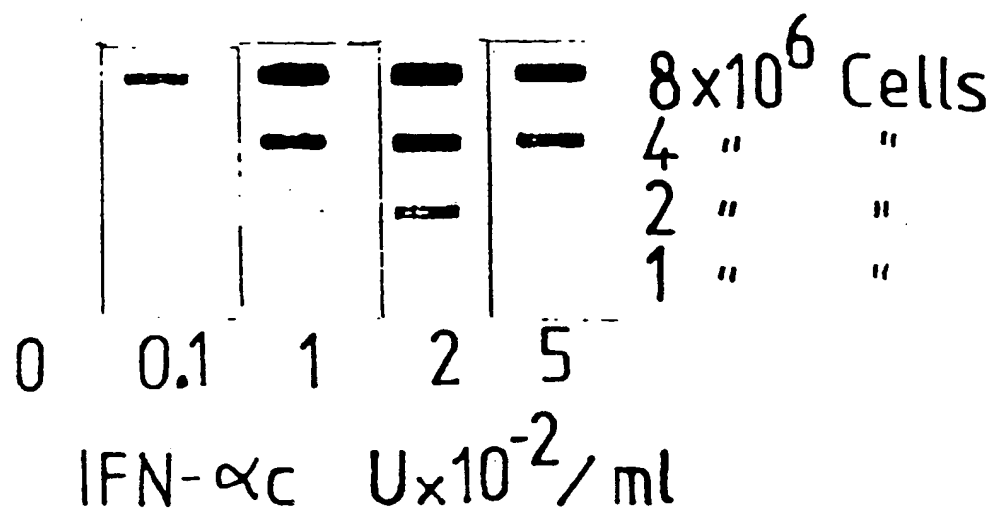


FIG. 15

SPECIFIC IMMUNOPRECIPITATION OF (2'-5') A SYNTHETASE ACTIVITY BY ANTI-PEPTIDE ANTIBODIES

ENZYME ACTIVITY IMMUNOPRECIPITATED FROM

DAUDI CELLS		WISH CELLS	
ANTI-B cpm	ANTI-C cpm	ANTI-B cpm	ANTI-C cpm
5,600	0	12,420	48,290

mean of three experiments

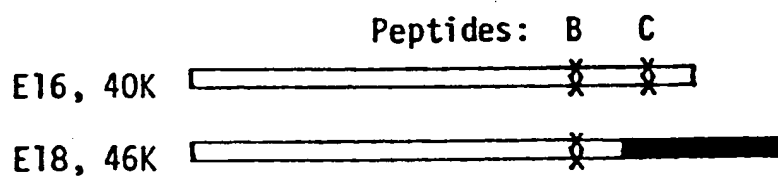
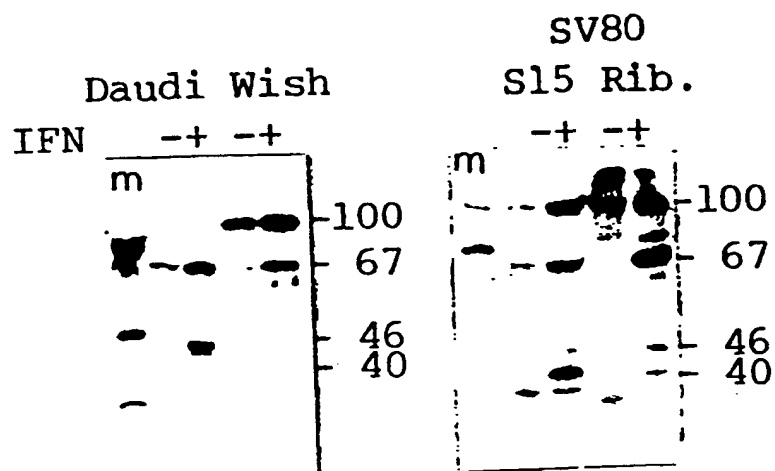


FIG.16

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Different forms of (2'-5') A synthetase in human cells and subfractions



Western blot
Anti OASE-B

FIG. 17

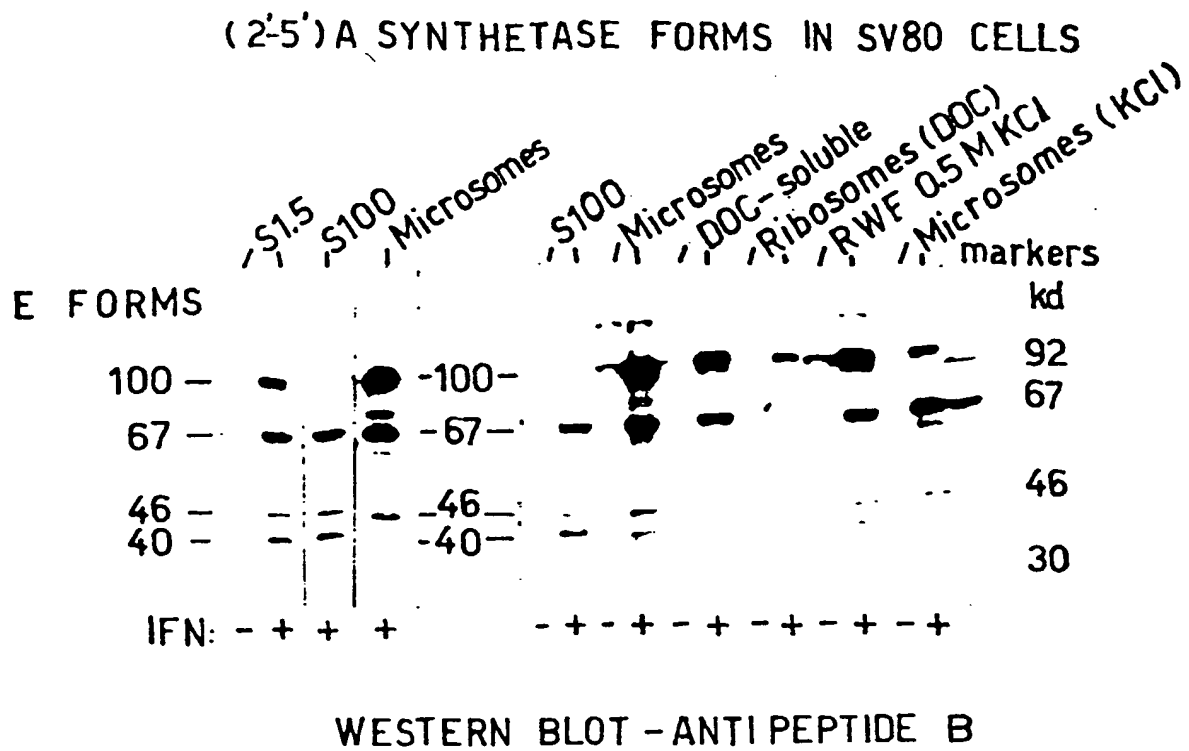


FIG. 18

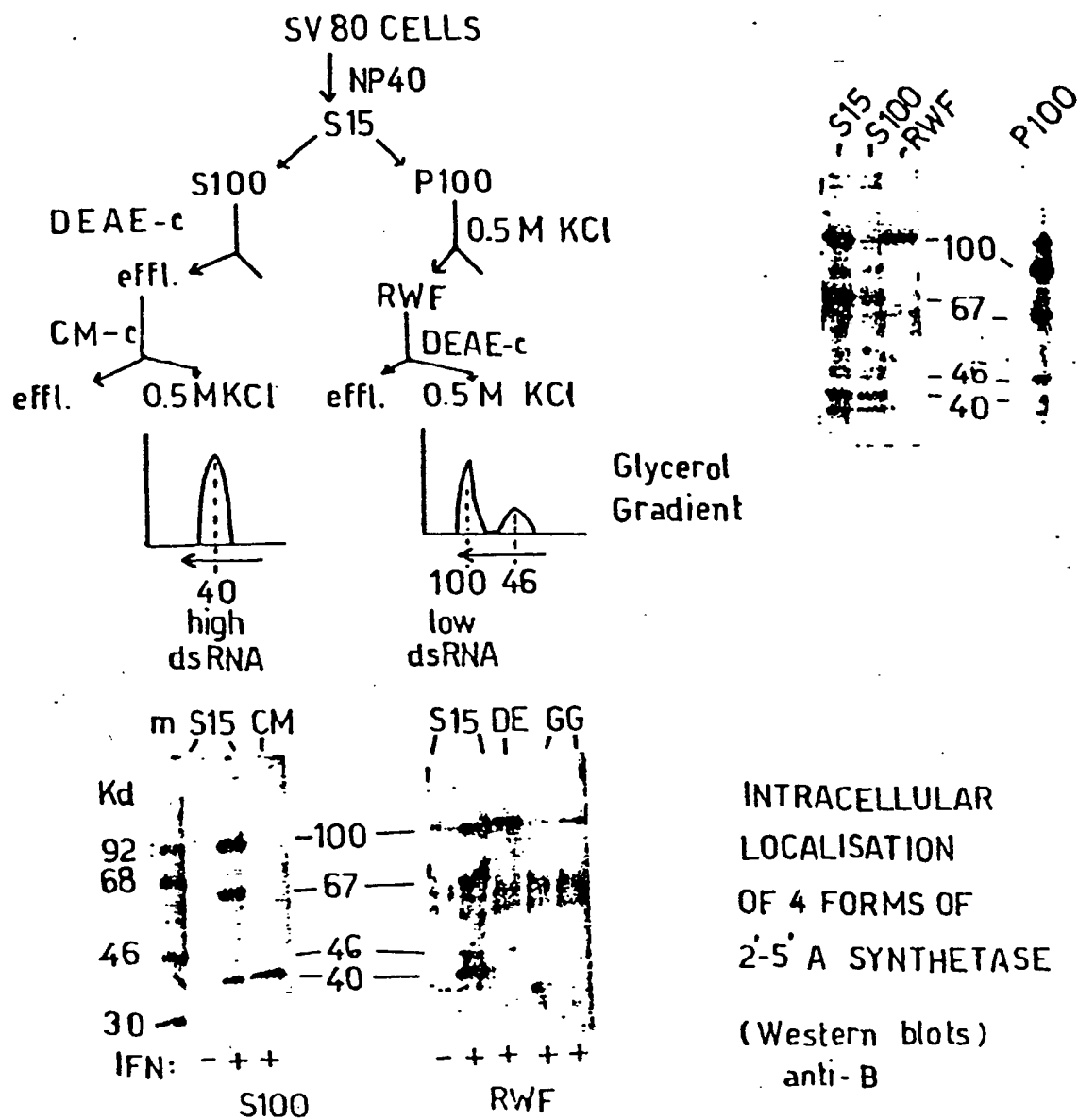
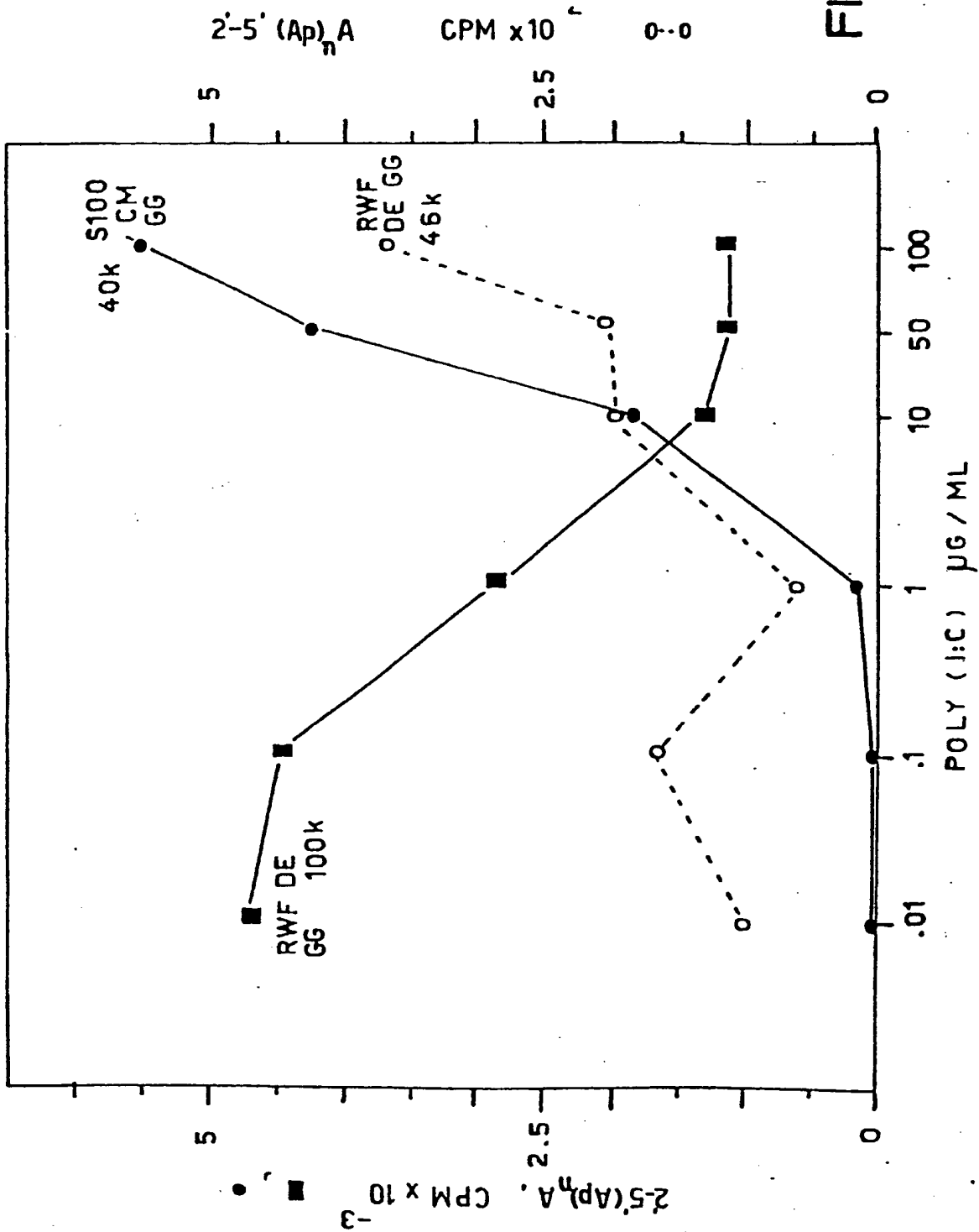


FIG.19

FIG. 20
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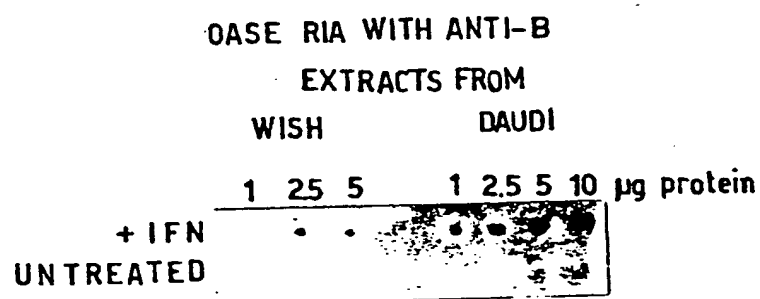


FIG. 21

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DIAGNOSIS OF VIRAL INFECTION BY IMMUNOFLUORESCENCE STAINING
OF PERIPHERAL BLOOD MONONUCLEAR CELLS WITH ANTI-OASE SERUM

Healthy Donor

Viral Disease

Normal serum*



Negative lymphocytes Positive lymphocytes* viral disease
Negative lymphocytes

FIG.22



European Patent
Office

EUROPEAN SEARCH REPORT

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Application number

DOCUMENTS CONSIDERED TO BE RELEVANT			EP 86111585.5
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl. 4)
P,X	THE EMBO JOURNAL, vol. 4, no. 9, 1985 (Oxford, GB) P. BENECH et al. "Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of human cells based on cDNAs and gene sequences" pages 2249-2256 * Totality * --	1-15, 25	C 12 N 15/00 C 07 H 21/04 C 07 H 21/02 C 12 N 1/20 C 12 N 9/00 C 12 Q 1/00 G 01 N 33/53 C 07 K 7/10 A 61 K 39/395
D,X	NUCLEIC ACIDS RESEARCH, vol. 13, no. 4, February 25, 1985 (Oxford, GB) P. BENECH et al. "3'End structure of the human (2'-5') oligo A synthetase gene; prediction of two distinct proteins with cell type-specific expression" pages 1267-1281 * Totality * --	1,6,7, 25	(C 12 N 1/20; C 12 R 1:19)
D,X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, vol. 80, no. 16, August 1983 (Baltimore, USA) G. MERLIN et al. "Molecular cloning and sequence of partial cDNA for interferon-induced (2'-5') oligo (A) synthetase mRNA from human cells" pages 4904-4908 * Totality * ----	1,25	TECHNICAL FIELDS SEARCHED (Int. Cl. 4) C 12 N C 07 H C 12 Q G 01 N C 07 K A 61 K
The present search report has been drawn up for all claims			
Place of search VIENNA		Date of completion of the search 01-12-1986	Examiner WOLF
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

CC Predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 11 A; 11 C; 15 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 50
 |||||
 Db 1 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 50

RESULT 2
 ID AAN70147
 ID AAN70147 standard; cDNA; 342 BP.

XX AAN70147;
 XX
 XX 18-APR-1991 (first entry)
 DT
 DE Sequence of cDNA clone C56 corresponding to an interferon-induced mRNA.
 XX
 XX In vivo interferon assay; ss.
 KW Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT CDS 1..201
 FT /*tag= a
 FT polyA_signal 322..328
 FT /*tag= c
 FT polyA_site 343
 FT /*tag= b
 XX
 XX EP217102-A.
 XX
 XX 08-APR-1987.
 XX
 XX 21-AUG-1986; 86EP-00111585.
 XX
 XX 28-AUG-1985; 85IL-000762233.
 PR 08-APR-1986; 86IL-00078445.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Revel M, Chebath J;
 XX WPI; 1987-095196/14.
 DR P-PSDB; AAP70093.
 XX
 XX Recombinant enzyme having (2'-5') oligo A synthetase activity - used for
 PT monitoring the response of a patient to an interferon.
 XX
 XX Example; Fig 4B; 90pp; English.

CC A partial cDNA clone (E1) for the OAS mRNA from human SV80 cells was
 CC first obd. through its ability to select by hybridisation a mRNA
 CC producing OAS activity upon translation in Xenopus laevis oocytes. The E1
 CC cDNA insert hybridises to 3RNA species of 1.6, 1.8 and 3.6 kb which are
 CC coincubed by IFN in SV80 cells. cDNA clones for the 1.6 and 1.8 RNAs have
 CC been isolated and sequenced
 XX
 SQ Sequence 342 BP; 108 A; 59 C; 66 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 1; Length 342;
 Best Local Similarity 100.0%; Pred. No. 2e-10;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 50
 |||||
 Db 154 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 203

RESULT 3
 AAT21101
 ID AAT21101 standard; cDNA to mRNA; 408 BP.

XX AAT21101;
 AC AAT21101;
 XX
 DT 16-JUL-1996 (first entry)
 XX
 DE Human gene signature HUMGS02403.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 XX Homo sapiens.

OS
 XX WO9514772-A1.
 PN
 XX 01-JUN-1995.
 PD
 XX
 XX 11-NOV-1994; 94WO-JP001916.
 XX
 XX 12-NOV-1993; 93JP-00355504.
 PR

XX (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 XX
 XX Matsubara K, Okubo K;
 PI WPI; 1995-206931/27.

XX
 XX Single-stranded DNA for identifying gene signatures - isolated from 3'-
 PT directed human cDNA library that reflects relative abundance of corresp.
 PT mRNA in specific human tissues.
 XX
 PS Claim 1; Page 800; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp. double
 CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in
 CC AAT19001-726937 and which is able to hybridise to part of human genomic
 CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
 CC obtained from 3'-directed cDNA libraries prepared from various human
 CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
 CC poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
 CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
 CC with specific mRNAs. Each library is constructed so as to reflect
 CC accurately the relative abundance of different mRNAs in the particular
 CC tissue from which it was derived. The appearance frequency of a given GS
 CC in a cDNA library can be determined (esp. using primers and probes
 CC derived from the GS sequences) as a means of diagnosing abnormal cell
 CC function or for recognising different cell types

SQ Sequence 408 BP; 133 A; 64 C; 80 G; 130 T; 0 U; 1 Other;

Query Match 100.0%; Score 50; DB 2; Length 408;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 50
 |||||
 Db 85 CTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAAGGTCCTTAGGC 134

RESULT 4
 ABV15983
 ID ABV15983 standard; cDNA; 418 BP.
 XX
 XX ABV15983;

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